

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:28:48 ; Search time 17 Seconds
(without alignments)
548.268 Million cell updates/sec

Title: US-10-C50-552A-2

Perfect score: 903

Sequence: 1 MAALQKSVSSFLMGTATSC.....EIKALGELDLFLFMSLRNACI 179

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897	99.3	179	1 IL22_HUMAN	Q9gx6 homo sapien
2	718	79.5	179	1 IL22_MOUSE	Q9jy9 mus musculus
3	714	79.1	179	1 IL22_MOUSE	Q9jy9 mus musculus
4	106.5	11.8	179	1 IL10_CEREL	P51746 cervus elap
5	105.5	11.7	178	1 IL10_MACFA	P79338 macaca fasc
6	103	11.4	170	1 BCRF_BEV	P03180 epstein-bar
7	101.5	11.2	178	1 IL10_CERTO	P46651 cercopithecus
8	101.5	11.0	183	1 MOB5_RAT	P51496 macaca mulia
9	99.5	11.0	178	1 IL10_HUMAN	Q9j124 rattus norv
10	96.5	10.7	178	1 IL10_HUMAN	P22301 homo sapien
11	96.5	10.7	178	1 IL10_MARMO	Q9jkh7 marmota mon
12	95.5	10.6	178	1 IL10_FELCA	P55029 felis silve
13	95.5	10.6	178	1 IL10_MACNE	P51497 macaca neme
14	95	10.5	178	1 IL10_BOVIN	P43480 bos taurus
15	93	10.3	174	1 IL10_TRIVU	Q97798 trichosurus
16	90.5	10.0	178	1 IL10_MOUSE	P18933 mus musculus
17	89.5	9.9	178	1 IL10_HORSE	Q28374 equus cabal
18	89.5	9.9	181	1 IL10_CANFA	P48411 canis faml
19	87	9.6	175	1 IL10_PIG	Q29055 sus scrofa
20	86	9.5	206	1 IL24_HUMAN	Q13007 homo sapien
21	85	9.4	177	1 IL10_SHEEP	Q29408 ovis aries
22	84.5	9.4	164	1 IL10_ORCOR	Q46673 orcinus orc
23	84.5	9.4	178	1 IL10_RAT	P29456 rattus norv
24	84	9.3	171	1 IL26_HUMAN	Q9nph9 homo sapien
25	82	9.1	2184	1 RRPL_CDOVO	P24658 canine dist
26	81.5	9.0	178	1 IL10_CAVPO	Q921y5 cavia porce
27	80	8.9	569	1 PVKD_PLAFA	Q08210 plasmodium
28	79.5	8.8	178	1 IL10_MERUN	P47965 meriones un
29	79.5	8.8	294	1 Y237_MYCGE	P47479 mycoplasma
30	79.5	8.8	1391	1 N157_YEAST	Q01433 saccharomyc
31	78.5	8.7	879	1 AMD2_HUMAN	Q01433 homo sapien
32	78	8.6	176	1 IL20_HUMAN	Q9nyy1 homo sapien
33	77	8.5	214	1 PITX_RHIME	O30498 rhizobium m

34 76 8.4 179 1 IL10_HSV2
35 76 8.4 245 1 UBIE_BACTIN
36 76 8.4 518 1 TT8_ARATH
37 75.5 8.4 691 1 EFG2_SYNY3
38 75 8.3 369 1 KAPR_STRPU
39 75 8.3 917 1 DML3_ARATH
40 74.5 8.3 430 1 PSBR_METJA
41 74.5 8.3 4451 1 GR5B_BACBR
42 74 8.2 439 1 SYH_CLOTE
43 74 8.2 553 1 MCRA_METJA
44 73.5 8.1 361 1 YG59_METJA
45 73.5 8.1 928 1 NIBA_HUMAN

ALIGNMENTS

RESULT 1
IL22_HUMAN STANDARD; PRT; 179 AA.
AC Q9GX6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-22 precursor (IL-22) (IL-10-related T-cell-derived
DE inducible factor) (IL-TIF) (UNQ3099/PRO10096).
GN IL22 OR ILTIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20420346; PubMed=10954742;
RA Dumoutier L., Van Roost E., Colau D., Renauld J.-C.;
RT "Human interleukin-10-related T cell-derived inducible factor:
RT molecular cloning and functional characterization as an hepatocyte-
RT stimulating factor";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10144-10149(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21069354; PubMed=11197690;
RA Dumoutier L., Van Roost E., Colau D., Ameye G., Michaux L.,
RA Renauld J.-C.;
RT "IL-TIF/IL-22: genomic organization and mapping of the human and mouse
RT genes";
RL Genes Immun. 1:488-494(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469498; PubMed=10875937;
RA Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
RA Wood W.I., Goddard A.D., Gurney A.L.;
RT "Interleukin (IL)-22, a novel human cytokine that signals through the
RT interferon receptor-related proteins CRF2-4 and IL-22R.";
RL J. Biol. Chem. 275:31335-31339(2000).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT GLY-158.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand K., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale

```

RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
CC in vivo.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ277247; CAC06085.1; -.
DR EMBL; AJ277248; CAC9409.1; -.
DR EMBL; AF279437; AAG22084.1; -.
DR EMBL; AF387519; AAK62468.1; -.
DR EMBL; AY358890; AQA9249.1; -.
DR GenBank; HGNC:14900; IL22.
DR MIM; 605330; -.
DR GO; GO:0005576; C:extracellular; IC.
DR GO; GO:0045518; F:interleukin-22 receptor binding; KAS.
DR GO; GO:0006953; P:acute-phase response; NAS.
DR GO; GO:0007267; P:cell-cell signaling; IC.
DR GO; GO:0006954; P:inflammatory response; NAS.
DR InterPro; IPR000098; Interleukin_10.
DR PROSITE; PS00520; INTERLEUKIN_10.
DR KW Cytokine; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 33
FT CHAIN 34 179
FT INTERLEUKIN-22.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 158 158 S->G
FT /FTId=VAR_013078.
FT SQ SEQUENCE 179 AA; 20011 MW; 3C35E64D60CF8767 CRC64;
Query Match 99.3%; Score 897; DB 1; Length 179;
Best Local Similarity 99.3%; Pred. No. 4.7e-78;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALQKSVSFLMGTATSCLLLLALLVQGGAAPISSHCHRLDKSNFQPYITNRTFMA 60
DB 1 MAALQKSVSFLMGTATSCLLLLALLVQGGAAPISSHCHRLDKSNFQPYITNRTFMA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLKMKVLMFTLEEVLPQSDRFQPMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLKMKVLMFTLEEVLPQSDRFQPMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHQRNVQKLDKTVKKIGSGEIKAIKGLDLPFMSLRNACI 179
DB 121 FIARISNRLSTCHIEGDDHLHQRNVQKLDKTVKKIGSGEIKAIKGLDLPFMSLRNACI 179
RESULT 2
IL22 MOUSE
ID IL22_MOUSE STANDARD; PRT; 179 AA.
AC Q9JUY9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-22 precursor (IL-22) (IL-10-related T-cell-derived
DE inducible factor) (IL-TIF) (IL-TIF alpha) (Interleukin-22a) (IL-22a).
GN IL22 OR IL22A OR ILTIFA OR ILTIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STAIN=AKR;
RX MEDLINE=20126044; PubMed=10657629;
RA Dumoutier L., Louahed J., Renauld J.-C.;
RT "Cloning and characterization of IL-10-related T cell-derived
RT inducible factor (IL-TIF), a novel cytokine structurally related to
RT IL-10 and inducible by IL-9";
RL J. Immunol. 164:1814-1819(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STAIN=129;
RX MEDLINE=21069354; PubMed=11197690;
RA Dumoutier L., Van Roost E., Colau D., Ameys G., Michaux L.,
RT Renauld J.-C.;
RT "IL-TIF/IL-22: genomic organization and mapping of the human and mouse
RT genes.";
RL Genes Immun. 1:488-494(2000).
CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
CC in vivo.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ249491; CAB75546.1; -.
DR EMBL; AJ294727; CAC19435.1; -.
DR MED; MG1:1355307; IL22.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.
DR GO; GO:0042516; P:regulation of tyrosine phosphorylation of S. . .; IDA.
DR InterPro; IPR000098; Interleukin_10.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 33
FT CHAIN 34 179
FT INTERLEUKIN-22.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 179 AA; 20106 MW; AC0F5574AA95274 CRC64;
Query Match 79.5%; Score 718; DB 1; Length 179;
Best Local Similarity 76.5%; Pred. No. 4.6e-61;
Matches 137; Conservative 22; Mismatches 20; Indels 0; Gaps 0;
QY 1 MAALQKSVSFLMGTATSCLLLLALLVQGGAAPISSHCHRLDKSNFQPYITNRTFMA 60
DB 1 MAALQKSVSFLMGTATSCLLLLALLVQGGAAPISSHCHRLDKSNFQPYITNRTFMA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLKMKVLMFTLEEVLPQSDRFQPMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSAKQCYLMKQVLMFTLEEVLPQSDRFQPMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHQRNVQKLDKTVKKIGSGEIKAIKGLDLPFMSLRNACI 179
DB 121 FLTKLSNQLSSCHISGDDQNKVRLKTKVKGSGEIKAIKGLDLPFMSLRNACV 179
RESULT 3
IL22 MOUSE
ID IL22_MOUSE STANDARD; PRT; 179 AA.
AC Q9JUY8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-22 precursor (IL-22b) (IL-10-related T-cell-derived
DE inducible factor beta) (IL-TIFb) (IL-TIF beta).
GN IL22B OR ILTIFB.

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
R2 SEQUENCE FROM N.A.
R3 STRAIN=129;
R4 MEDLINE=20126044; PubMed=10657629;
R5 Dumoutier L., Louahed J., Renaud J.-C.;
R6 "Cloning and characterization of IL-10-related T cell-derived
R7 inducible factor (IL-TIF), a novel cytokine structurally related to
R8 IL-10 and inducible by IL-9";
R9 J. Immunol. 164:1814-1819 (2000).
RN [2]
R2 SEQUENCE FROM N.A.
R3 STRAIN=129;
R4 MEDLINE=21069354; PubMed=11197690;
R5 Dumoutier L., Van Roost E., Colau D., Amey G., Michaux L.,
R6 "IL-TIF/IL-22: genomic organization and mapping of the human and mouse
R7 genes";
R8 Genes Immun. 1:488-494 (2000).
RL Genes Immun. 1:488-494 (2000).
CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
CC in vivo.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; AJ249492; CAB75547.1; -.
DR EMBL; AJ294728; CACJ9436.1; -.
DR MGI; 2151139; Il10f.
DR InterPro; IPR000098; Interleukin_10.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 179 INTERLEUKIN-22B.
FT CARBOHYD 54 54 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 63 68 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLNAC. . .) (POTENTIAL).
SQ SEQUENCE 179 AA; 20162 MW; 4425496580DA5F60 CRC64;

Query Match 79.1%; Score 714; DB 1; Length 179;
Best Local Similarity 76.0%; Pred. No. 1.1e-60;
Matches 136; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTATLSCILLALLVQGGAAAPISSHCRDLKSNFOQPYITNRTFMLA 60
Dd 1 MAVLQKSVSFLMGTATLSCILLALLVQGGAAAPISSHCRDLKSNFOQPYITNRTFMLA 60

QY 61 KEASLADNNTDVRLLGKFLGVMSERCYLMQVINTFLTEVLFPQSDRFQPMQVVP 120
Dd 61 KEASLADNNTDVRLLGKFLGVMSERCYLMQVINTFLTEVLFPQSDRFQPMQVVP 120

QY 121 FIARISRLSCTHGGDHLHQNVOKLQDTVKKIGESGEIKAGELDLFLF 179
Dd 121 FLTKLSGLSCHSGDDQNIQKVRUKETVKKIGESGEIKAGELDLFLFMSLRNACV 179

RESULT 4
IL10 CEREL
ID IL10 CEREL STANDARD; PRT; 179 AA.
AC F51746;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DS Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory

```

```

DE factor) (CSIF).
GN IL10.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
R2 SEQUENCE FROM N.A.
R3 MEDLINE=96063015; PubMed=7579578;
R4 Lockhart B., Slobbe L., Droogmans L., Griffin F., Buchan G.;
R5 "The cloning and sequencing of cervine interleukin 10.";
R6 DNA Seq. 5:265-268 (1995).
R7 -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
R8 including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
R9 activated macrophages and by helper T cells (By similarity).
R10 -!- SUBUNIT: Homodimer (By similarity).
R11 -!- SUBCELLULAR LOCATION: Secreted.
R12 -!- SIMILARITY: Belongs to the IL-10 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; U11767; AAA85434.1; -.
DR HSP; P22301; 1INR.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005141; F:interleukin-10 receptor binding; NAS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTLEUKIN10.
DR ProDom; PD003887; Interleukin_10; 1.
DR SMART; SM00189; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 179 INTERLEUKIN-10.
FT DISULFID 31 127 BY SIMILARITY.
FT DISULFID 81 133 BY SIMILARITY.
FT CARBOHYD 135 135 N-LINKED (GLNAC. . .) (POTENTIAL).
SQ SEQUENCE 179 AA; 20467 MW; A1C0035D484B050 CRC64;

Query Match 11.8%; Score 106.5; DB 1; Length 179;
Best Local Similarity 22.8%; Pred. No. 0.0051;
Matches 41; Conservative 32; Mismatches 74; Indels 33; Gaps 6;

QY 20 CILLAL-LLVQGGAAAPISSHCRDLKSNFOQPYITNRTFMLAKEASLA-----DM 68
Dd 10 CLVFLAGVAASRDASAPSDSC-----THFSNLSPLMLRELRTAFSRVKNFFQMKD 60

QY 69 NTVRLVIGEKFLGVMSERCYLMQVINTFLTEVLFPQSDRFQPMQVVPFIAR---- 124
Dd 61 QLDLSMLLTQSLDDPKYLIGQALSEMIQFVLEVM-POAENHGPRIKEHVNLSGEKLT 119

QY 125 ISNRLSTCHIBGDDHLHQNVOKLQDTVKKIGESGEIKAGELDLFLF-----MSLRN 176
Dd 120 LRLRRCRFLPCENKSKAVEQKSVFSKQGVYKAMSEFDIYNIYIYTTMKMN 179

RESULT 5
IL10 MACFA
ID IL10 MACFA STANDARD; PRT; 178 AA.
AC P79338;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DS Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory

```

```

DE factor) (CSIF).
GN IL10.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
CC including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
CC activated macrophages and by helper T cells (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL; AB000514; BAA19132.1; -.
DR HSP; P22301; 11NR.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0008189; F:apoptosis inhibitor activity; ISS.
* DR GO; GO:0005141; F:interleukin-10 receptor binding; ISS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0030183; P:B-cell differentiation; ISS.
DR GO; GO:0042100; P:B-cell proliferation; ISS.
DR GO; GO:0007253; P:cytoplasmic sequestration of NF-kappaB; ISS.
* DR GO; GO:0030097; P:hemopoiesis; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0045077; P:negative regulation of interferon-gamma bio. . .; ISS.
DR GO; GO:0045347; P:negative regulation of MHC class II biosynt. . .; ISS.
DR GO; GO:0045019; P:negative regulation of nitric oxide biosynt. . .; ISS.
DR GO; GO:0042130; P:negative regulation of T-cell proliferation; ISS.
DR GO; GO:0045191; P:regulation of isotype switching; ISS.
DR GO; GO:0042092; P:T-helper 2 type immune response; ISS.
DR GO; GO:0007260; P:tyrosine phosphorylation of STAT protein; ISS.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 178 INTERLEUKIN-10.
FT DISULFID 30 126 BY SIMILARITY.
FT DISULFID 80 132 BY SIMILARITY.
FT CARBOHYD 134 134 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 178 AA; 20585 MW; 35CEDD9B3B9A718 CRC64;

Query Match 11.7%; Score 105.5; DB 1; Length 178;
Best Local Similarity 23.5%; Pred. No. 0.0063;
Matches 43; Conservative 32; Mismatches 77; Indels 31; Gaps 6;

QY 18 TSCLLJLALVQGAAP-----ISSHRLDKSN-----FOOPYITNTEPLAKEASL 65
Db 3 SSALLCCVLLTVGRASPGQGTGSENSCTFPGNLPMLRLDLRDAFSRVKTFQMKD--- 59
QY 66 ADNNVTRLGKLFHGVSMSECYLMKVNLFTLEEVLPFPDRFPQYQVQVVPFIAR- 124
Db 60 ---QLDNILKESLLEDFKGLGQALSEMIQFLEVM-PQENHDPDKHGVNSLGEN 115
QY 125 ---ISMRESPTCHIEGDLHTQRNVQKDKOTVKKIGESGEIKATGELDL-----LFMS 173
Db 116 LKTLRLRLRCHRFPCENSKSKAVEQVKNFASKLQKGVYKAMSEFDIFINYEAVMTK 175

```

```

QY 174 LRN 176
Db 176 LRN 178

RESULT 6
ID BCRF_EBV STANDARD; PRT; 170 AA.
AC P03180;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE BCRF1 protein precursor (20 kDa protein).
GN BCRF1.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP PROTEIN CODING REGION.
RA MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RA "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211 (1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86045995; PubMed=2998073;
RX Hudson G.S., Bankier A.T., Satchwell S.C., Barrell B.G.;
RX "The short unique region of the B95-8 Epstein-Barr virus genome.";
RL Virology 147:81-98 (1985).
RN [3]
RP FUNCTION.
RX MEDLINE=90273182; PubMed=2161559;
RX Moore K.W., Vieira P., Fiorentino D.F., Trounstein M.L.,
RX Khan T.A., Mosmann T.R.;
RX "Homology of cytokine synthesis inhibitory factor (IL-10) to the
RX Epstein-Barr virus gene BCRF1.";
RL Science 248:1230-1234 (1990).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=97303052; PubMed=9159483;
RX Zdanov A., Schalk-Hihi C., Menon S., Moore K.W., Wlodawer A.;
RX "Crystal structure of Epstein-Barr virus protein BCRF1, a homolog of
RX cellular interleukin-10.";
RL J. Mol. Biol. 268:460-467 (1997).
CC -!- FUNCTION: INHIBITS IFN-GAMMA SYNTHESIS.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -!- CAUTION: THERE ARE 2 BCRF1 GENES. ONE IS WRITTEN WITH A LOWER
CC CASE C (B(CRF1)) AND THE OTHER WITH A CAPITAL C (BCRF1).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL; V01555; CAA24863.1; -.
DR EMBL; M11924; AAA45900.1; -.
DR PIR; A03741; Q0BE2.
DR PDB; 1VLK; 01-APR-97.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.

```


CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@sb-sib.ch).

CC -----
 DR EMBL; L26029; AAA99975.1; --
 DR HSSP; P22301; 2ILK.
 DR GO; GO:0005576; C:extracellular; ISS.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; ISS.
 DR GO; GO:0005141; F:interleukin-10 receptor binding; ISS.
 DR GO; GO:0006916; P:anti-apoptosis; ISS.
 DR GO; GO:0030183; P:B-cell differentiation; ISS.
 DR GO; GO:0042100; P:B-cell proliferation; ISS.
 DR GO; GO:0007253; P:cytoplasmic sequestration of NF-kappaB; ISS.
 DR GO; GO:0030957; P:hemopoiesis; ISS.
 DR GO; GO:0006954; P:inflammatory response; ISS.
 DR GO; GO:0045077; P:negative regulation of MHC class II biosynt. . . ; ISS.
 DR GO; GO:0045347; P:negative regulation of nitric oxide biosynt. . . ; ISS.
 DR GO; GO:0045019; P:negative regulation of T-cell proliferation; ISS.
 DR GO; GO:0042100; P:negative regulation of T-cell proliferation; ISS.
 DR GO; GO:0045191; P:regulation of isotype switching; ISS.
 DR GO; GO:0042092; P:T-helper 2 type immune response; ISS.
 DR GO; GO:0007260; P:tyrosine phosphorylation of STAT protein; ISS.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PRINTS; PR01294; INTRLEUKIN10.
 DR ProDom; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN 10; 1.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 178 INTERLEUKIN-10.
 FT DISULFID 30 126 BY SIMILARITY.
 FT DISULFID 80 132 BY SIMILARITY.
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 178 AA; 20557 MW; 35CCDD98B38A718 CRC64;

Query Match 11.2%; Score 101.5; DB 1; Length 178;
 Best Local Similarity 23.8%; Pred. No. 0.015;
 Matches 40; Conservative 30; Mismatches 75; Indels 23; Gaps 5;
 QY 18 TSCILLALLVGGGAAP-----ISSHCRLDKSN-----FQPYITNRTFMLEKASL 65
 DB 3 SSALLCCVLLTGVRASPGOGTSENCTFPCNLPMLDLRDAFVRKTFQMKD--- 59
 QY 66 ANNTDVLIGELKFGVSMSECYLMKQVNTLEVLFPQSDRFQPMQVVPFTAR- 124
 DB 60 ---QLDNLLKESLLEDPKGLGCGCALSEMIQYLEEW-POENHDPDIKEHVNSLGEN 115
 QY 125 ---ISRLSTCHIEGDDLHIQNVOKLQDVKVIGSGEIKAGELDL 169
 DB 116 LKTLRLRLRCHRFLECNKSKAVEQVKNAPFKLQKGVYKAMSEFDI 163

RESULT 9
 MOBS RAT
 ID MCB5 RAT STANDARD; PRT; 183 AA.
 AC Q9J124;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytokine-like protein Mob-5 precursor.
 GN MOB5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20387329; PubMed=10825166;
 RA Zhang R.; Tan Z.; Liang P.;
 RT "Identification of a novel ligand-receptor pair constitutively

RT activated by ras oncogenes.";
 RL J. Biol. Chem. 275:24436-24443 (2000).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@sb-sib.ch).

DR EMBL; AF269251; AAF75553.1; --
 DR InterPro; IPR000098; Interleukin_10.
 DR ProDom; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN 10; 1.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 183 CYTOKINE-LIKE PROTEIN MOB-5.
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 183 AA; 21096 MW; AF7A11466C491AC4 CRC64;

Query Match 11.0%; Score 99.5; DB 1; Length 183;
 Best Local Similarity 27.7%; Pred. No. 0.024;
 Matches 36; Conservative 19; Mismatches 44; Indels 31; Gaps 5;
 QY 67 DNNTDVLIGELKFGVSMSECYLMKQVNTLEVLFPQSDRFQPMQVVPFTARIS 126
 DB 61 DELTSVELLKPQVLQNVSDAESCYLAHSLKFLYNTV-----FQVYSHKVPF--KVL 111
 QY 127 NRLSTCHIEGDDLHIQNVOKLQD-----TVKKIG-ESGELKAGE 166
 DB 112 KSFTT--LANNFLVIMSKLPQSKDNAMLPISDSARRRFLYHRTFKQLDIEVALAKAFGE 169
 QY 167 LDLEFSLRN 176
 DB 170 VDILLAWQN 179

RESULT 10
 IL10 HUMAN
 ID IL10 HUMAN STANDARD; PRT; 178 AA.
 AC 222301;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory
 DB factor) (CSIF).
 GN IL10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=91142134; PubMed=1847510;
 RA Vieira P.; de Waal-Malefyt R.; Dang M.-N.; Johnson K.E.; Kastelein R.;
 RA Fiorentino D.F.; Devries J.E.; Roncarolo M.-G.; Mosmann T.R.;
 RA Moore K.W.;
 RT "Isolation and expression of human cytokine synthesis inhibitory
 factor cDNA clones: homology to Epstein-Barr virus open reading frame
 RT BCRF1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1172-1176 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sanjanwalla B.; de Waal-Malefyt R.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Dai W.-J.; Jiang H.-C.; Fan S.-H.;

Query Match 10.7%; Score 96.5; DB 1; Length 178;
 Best Local Similarity 22.4%; Pred. No. 0.045;
 Matches 41; Conservative 33; Mismatches 78; Indels 31; Gaps 6;

QY 18 TSCLLILALVQSGAAP-----ISSHCLDKSN-----FQCPYITNTEFMLEKASL 65
 DB 3 SSALLCCVLVTGVRASPGQSTGSENCSTHPPGNLPLNMLDLRDAFSRVKTFQMKD--- 59
 QY 66 ADNNTDVLGEGKLFHGVSMSERCYLMQVINFTELVLPFQSDRFPQ-----YMQEVVVF 121
 DB 60 ---QLNLLKLSLEDPKGLGCOALSEMIOFYLEVM-POAENQDPDKAHVNSLGEN 115
 QY 122 IARISNRLSTCHIEGDDLHQRNVOKLQVTKKIGESGKAIKAGELDL-----LPM 173
 DB 116 LKTLRLRCHRFPCENKSKAVEQVKNFKNLQKGIYKAMSEFDIFINYEAVYTMK 175
 QY 174 LRN 176
 DB 176 IRN 178

RESULT 11

IL10 MARMO STANDARD; PRT; 178 AA.
 AC Q9JHK7; 2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF).
 GN IL10 OR IL-10.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae; Marmota.
 OC NCBI_TaxID=9995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Periphereal blood;
 RA Li D.H., Cullen J.M.;
 RT "The woodchuck interleukin-10 gene: cloning and structural analysis."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; AF012909; AAF34862.1; -
 CC EMBL; AF120030; AAF28855.1; -
 CC HSSP; P22301; 1INR
 CC GO; GO:0005576; C:extracellular; ISS.
 CC GO; GO:0008189; F:apoptosis inhibitor activity; ISS.
 CC GO; GO:0005141; F:interleukin-10 receptor binding; ISS.
 CC GO; GO:0006916; P:anti-apoptosis; ISS.
 CC GO; GO:0030183; P:B-cell proliferation; ISS.
 CC GO; GO:0042100; P:B-cell differentiation; ISS.
 CC GO; GO:0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
 CC GO; GO:0030097; P:hemopoiesis; ISS.
 CC GO; GO:0006954; P:inflammatory response; ISS.
 CC GO; GO:0045077; P:negative regulation of interferon-gamma bio. .; ISS.
 CC GO; GO:0045347; P:negative regulation of MHC class II biosynt. .; ISS.

DR GO; GO:0045019; P:negative regulation of nitric oxide biosynt. .; ISS.
 DR GO; GO:0042130; P:negative regulation of T-cell proliferation; ISS.
 DR GO; GO:0045191; P:regulation of isotype switching; ISS.
 DR GO; GO:0042092; P:T-helper 2 type immune response; ISS.
 DR GO; GO:0007260; P:tyrosine phosphorylation of STAT protein; ISS.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PRINTS; PR01294; Interleukin10.
 DR PRODOM; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 178 INTERLEUKIN-10.
 FT DISULFID 30 126 BY SIMILARITY.
 FT DISULFID 80 132 BY SIMILARITY.
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 178 AA; 20371 MW; 235B30ACE4CF82A2 CRC64;

Query Match 10.7%; Score 96.5; DB 1; Length 178;
 Best Local Similarity 28.2%; Pred. No. 0.045;
 Matches 29; Conservative 19; Mismatches 50; Indels 5; Gaps 2;

QY 71 DVRLIGEKLFHGVSMSERCYLMQVINFTELVLPFQSDRFPQYMQEVVVPPIAR-----IS 126
 DB 62 DMLLSESLLEDPKGLGCOALSEMIOFYLEVM-POAENSPDVKHNSLGEKLTIR 120
 QY 127 NRLSTCHIEGDDLHQRNVOKLQVTKKIGESGKAIKAGELDL 169
 DB 121 LRLRCHRFPCENKSKAVEQVKNFKNLQKGIYKAMSEFDI 163

RESULT 12

IL10 FELCA STANDARD; PRT; 178 AA.
 AC P55029;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF).
 GN IL10.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OC NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Scott B.M., O'Reilly K.L.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; U39569; AAA81771.1; -
 CC HSSP; P22301; 1INR
 CC GO; GO:0005576; C:extracellular; ISS.
 CC GO; GO:0008189; F:apoptosis inhibitor activity; ISS.
 CC GO; GO:0005141; F:interleukin-10 receptor binding; ISS.
 CC GO; GO:0006916; P:anti-apoptosis; ISS.
 CC GO; GO:0030183; P:B-cell differentiation; ISS.
 CC GO; GO:0042100; P:B-cell proliferation; ISS.


```

DR GO: 0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
DR GO: 00030037; P:hemoipoiesis; ISS.
DR GO: 0006954; P:inflammatory response; ISS.
DR GO: 00045077; P:negative regulation of interferon-gamma bio. . .; ISS.
DR GO: 00045347; P:negative regulation of MHC class II biosynt. . .; ISS.
DR GO: 00045019; P:negative regulation of nitric oxide biosynt. . .; ISS.
DR GO: 00042130; P:negative regulation of T-cell proliferation; ISS.
DR GO: 00045131; P:negative regulation of isotype switching; ISS.
DR GO: 00042032; P:T-helper 2 type immune response; ISS.
DR GO: 0007260; P:tyrosine phosphorylation of STAT protein; ISS.
DR InterPro: IPR000398; Interleukin_10.
DR Pfam: PF00726; IL10; 1.
DR PRINTS: PR01294; INTRLEUKIN10.
DR ProDom: PD003687; Interleukin_10; 1.
DR SMART: SM00188; IL10; 1.
DR PROSITE: PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 178 INTERLEUKIN-10.
FT DISULFID 30 126 BY SIMILARITY.
FT DISULFID 80 132 BY SIMILARITY.
FT CARBOHYD 29 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 178 AA; 20529 MW; 836C9635D9C185AA CRC64;

Query Match 10.6%; Score 95.5; DB 1; Length 178;
Best Local Similarity 23.4%; Pred. No. 0.056;
Matches 25; Conservative 20; Mismatches 35; Indels 5; Gaps 2;

QY 89 CYLMKQVLFLEVLFPQSDRFQYMOEVVPPFIAR----ISNRLSTCHIEGDDLHIQRN 144
D 80 CQALSEMIQFVLEVM-PQAEENEDFIQVNSLGEKLTLLRLRCHRFPLPCNKSKV 138
* QY 145 VQKLKDTVKKIGSGEIKAIQELDL 169
D 139 VEQVKSTPFSKLQKGVYKAMGEFDI 163

* RESULT 13
IL10_MACNE STANDARD; PRT; 178 AA.
ID IL10_MACNE
AC F51497;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF).
DE IL10.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PT 10000;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC !- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity).
CC !- SUBUNIT: Homodimer (By similarity).
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- SIMILARITY: Belongs to the IL-10 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

```

```

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L26031; AAA99976.1; -.
CC HSP: P22301; IINK.
DR GO: 0005576; C:extracellular; ISS.
DR GO: 0008189; P:apoptosis inhibitor activity; ISS.
DR GO: 0005141; P:interleukin-10 receptor binding; ISS.
DR GO: 0006916; P:anti-apoptosis; ISS.
DR GO: 0030183; P:B-cell differentiation; ISS.
DR GO: 0042100; P:B-cell proliferation; ISS.
DR GO: 0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
DR GO: 00030097; P:hemoipoiesis; ISS.
DR GO: 0006954; P:inflammatory response; ISS.
DR GO: 00045077; P:negative regulation of interferon-gamma bio. . .; ISS.
DR GO: 00045347; P:negative regulation of MHC class II biosynt. . .; ISS.
DR GO: 00045019; P:negative regulation of nitric oxide biosynt. . .; ISS.
DR GO: 00042130; P:negative regulation of T-cell proliferation; ISS.
DR GO: 00045131; P:negative regulation of isotype switching; ISS.
DR GO: 0007260; P:T-helper 2 type immune response; ISS.
DR InterPro: IPR000098; Interleukin_10.
DR Pfam: PF00726; IL10; 1.
DR PRINTS: PR01294; INTRLEUKIN10.
DR ProDom: PD003687; Interleukin_10; 1.
DR SMART: SM00188; IL10; 1.
DR PROSITE: PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 178 INTERLEUKIN-10.
FT DISULFID 30 126 BY SIMILARITY.
FT DISULFID 80 132 BY SIMILARITY.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 178 AA; 20560 MW; 35CC0D9D49E70718 CRC64;

Query Match 10.6%; Score 95.5; DB 1; Length 178;
Best Local Similarity 23.2%; Pred. No. 0.056;
Matches 39; Conservative 30; Mismatches 76; Indels 23; Gaps 5;

QY 18 TSCLLALLAVQGGAAAP-----ISSHCLDKSN-----FQPYITNRTFMLEASL 65
D 3 SSALLCCVLVTGVRASPGQGTQSENCTRPFGNLPMLRLDRDAFSKVTFFQMKD--- 59
QY 66 ADNNTDVRLLGEKLFHGVSMSERCYLMKQVINFLEVLFPQSDRFQYMOEVVPPFIAR- 124
D 60 ---QLDMILLKESLLEDFKVLGCGQALSEMIQFVLEVM-PQAEHDPDIKEHNSLGEN 115
QY 125 ---ISNRLSTCHIEGDDLHIQRNQVKLQDTVKKIGSGEIKAIQELDL 169
D 116 LKTLRLRLRCHRFPLPCNKSKAVEQVMNAFSLQKGVYKAMGEFDI 163

RESULT 14
IL10_BOVIN STANDARD; PRT; 178 AA.
ID IL10_BOVIN
AC P43480;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF).
DE IL10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Charolais; TISSUE=Blood;
RX MEDLINE=94156210; PubMed=8112615;
RA Hash S.M., Brown W.C., Rice-Ficht A.C.;
RT "Characterization of a cDNA encoding bovine interleukin 10: kinetics

```

of expression in bovine lymphocytes.";
 Gene 138:257-261 (1994).
 CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
 CC including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
 CC activated macrophages and by helper T cells (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U00799; AAA19011.1; -;
 CC HSPSP; P22301; LINR.
 CC GO; GO:0005576; C:extracellular; ISS.
 CC GO; GO:0008189; F:apoptosis inhibitor activity; ISS.
 CC GO; GO:0005441; F:interleukin-10 receptor binding; ISS.
 CC GO; GO:0006916; P:anti-apoptosis; ISS.
 CC GO; GO:0030153; P:B-cell differentiation; ISS.
 CC GO; GO:0042100; P:B-cell proliferation; ISS.
 CC GO; GO:0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
 CC GO; GO:0030097; P:hemopoiesis; ISS.
 CC GO; GO:0006954; P:inflammatory response; ISS.
 CC GO; GO:0042095; P:interferon-gamma biosynthesis; IMP.
 CC GO; GO:0045077; P:negative regulation of interferon-gamma bio. .; NAS.
 CC GO; GO:0045347; P:negative regulation of MHC class II biosynt. .; ISS.
 CC GO; GO:0045019; P:negative regulation of nitric oxide biosynt. .; NAS.
 CC GO; GO:0042130; P:negative regulation of T-cell proliferation; ISS.
 CC GO; GO:0045191; P:negative regulation of isotype switching; ISS.
 CC GO; GO:0042092; P:regulation of 2 type immune response; ISS.
 CC InterPro; IPR000098; Interleukin_10.
 CC Pfam; PF00726; IL10; 1.
 CC PRINTS; PR01294; INTRLEUKIN10.
 CC ProDom; PD003687; Interleukin_10; 1.
 CC SMART; SM00188; IL10; 1.
 CC PROSITE; PS00520; INTERLEUKIN_10; 1.
 CC Cytokine; Glycoprotein; Signal.
 CC FT CHAIN 1 18 POTENTIAL.
 CC FT CHAIN 19 178 INTERLEUKIN-10.
 CC FT DISULFID 30 126 BY SIMILARITY.
 CC FT DISULFID 80 132 BY SIMILARITY.
 CC FT CARBOHYD 134 134 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 178 AA; 20411 MW; 246D176BD9D056 CRC64;
 CC
 CC Query Match 10.5%; Score 95; DB 1; Length 178;
 CC Best Local Similarity 24.1%; Pred. No. 0.062;
 CC Matches 40; Conservative 32; Mismatches 74; Indels 20; Gaps 6;
 CC
 CC QY 19 SCILLALLVQGAAPISSHCHRLDKSNFQPPYITNRTFMALAK-EASLADNNTDVRIGE 77
 CC Db 3 SSALLCLVFLAGVAASRDASTLSDSSCTHLP--TSLPHMLRELRAAFGEAKTFQW--K 58
 CC
 CC QY 78 KLPHGVGSMSEK-----CYLMKQVNLFTLEVLFPQSDRFQPMQEVVPFIAR--- 124
 CC Db 59 DQHSLLLTQSLLDDPKGLVGCQALSEMIQFYLEEVM-PQAEHNGPDIDKEHVNLSGLK 117
 CC
 CC QY 125 -ISNRLSTCHIEGDLHIGRNQVKLQKDTVKKIGESGKKAIGELD 169
 CC Db 118 TLRLR-LRRCHRLFPCNKSKAVEKVEFSEIQGVYKAMSEFDI 163
 CC
 CC RESULT 15
 CC ID IL10 TRIVU STANDARD; PRT; 174 AA.
 CC AC Q97798;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)

Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF).
 DE IL10.
 GN Trichosurus vulpecula (Brush-tailed possum).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 CC NCBI_TaxID=9337;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99449065; PubMed=10520755;
 RA Medlock D.N., Aldwell F.E., Buddle B.M.;
 RT "Nucleotide sequence of a marsupial interleukin-10 cDNA from the
 CC Australian brushtail possum (Trichosurus vulpecula).";
 RT DNA Seq. 9:239-244 (1998).
 CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
 CC activated macrophages and by helper T cells (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-10 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF026277; AA001799.1; -;
 CC HSPSP; P22301; LINR.
 CC InterPro; IPR000098; Interleukin_10.
 CC Pfam; PF00726; IL10; 1.
 CC PRINTS; PR01294; INTRLEUKIN10.
 CC ProDom; PD003687; Interleukin_10; 1.
 CC SMART; SM00188; IL10; 1.
 CC PROSITE; PS00520; INTERLEUKIN_10; 1.
 CC Cytokine; Glycoprotein; Signal.
 CC FT SIGNAL 1 16 POTENTIAL.
 CC FT CHAIN 17 174 INTERLEUKIN-10.
 CC FT DISULFID 26 122 BY SIMILARITY.
 CC FT DISULFID 76 128 BY SIMILARITY.
 CC FT CARBOHYD 17 17 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 174 AA; 20262 MW; DA838DBF74DF9C06 CRC64;
 CC
 CC Query Match 10.3%; Score 93; DB 1; Length 174;
 CC Best Local Similarity 22.2%; Pred. No. 0.094;
 CC Matches 35; Conservative 37; Mismatches 74; Indels 12; Gaps 6;
 CC
 CC QY 21 LLLALL--VQGAAPISSHCHRLDKSNFQPPYITNRTFMALAK-EASLADNNTDVRIGE 77
 CC Db 5 MLFLCCLCVTSNLSALEDNCKTFTSTLPNMLRELRAAFSSVKTYFQTRDKLETKLIDK 64
 CC
 CC QY 78 KLPHGVGSMSEKCYLMKQVNLFTLEVLFPQSDRFQPMQEVVPFIAR---ISNRLSTCH 133
 CC Db 65 SLLEELKSVLGCQALSEMIQFYLEEVM-PQAEHNGPDIDKEHVNLSGLKALRLKRC 123
 CC
 CC QY 134 --IEGDLHIGRNQVKLQKDTVKKIGESGKKAIGELD 169
 CC Db 124 RELPCED--NSRWVKQVRNTYKELQGVYKAMGDFDI 159
 CC
 CC Search completed: June 30, 2004, 19:34:35
 CC Job time : 19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:32:59 ; Search time 41 Seconds
(without alignments)
1377.50% Million cell updates/sec

Title: US-10-050-552A-2
Perfect score: 903
Sequence: 1 MAALQKSYSSFLMGLTASC.....EIKATGELDLPLMSLRNACI 179

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: :017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116.5	12.9	175	13 Q7SX60	Q7sx60 tetraodon n
2	111.5	12.3	183	13 Q802T4	Q802t4 fugu rubrip
3	106.5	11.8	178	11 Q80WE8	Q80we8 peromyscus
4	106	11.7	181	13 Q7SX82	Q7sx82 tetraodon n
5	104	11.5	177	12 Q8UJ36	Q8uj36 cercopithec
6	99.5	11.0	171	12 Q9Q5L1	Q9q5l1 herpesvirus
7	98.5	10.9	178	6 Q8MKG9	Q8mkg9 salmisi sci
8	97.5	10.8	220	11 Q925J3	Q925j3 mus musculus
9	97	10.7	184	13 Q7ZSY8	Q7zsy8 tetraodon n
10	96	10.6	180	13 Q7T3I1	Q7t3i1 cyprinus ca
11	95.5	10.6	178	6 Q9TSJ7	Q9tsj7 felis silve
12	95.5	10.6	181	11 Q925S4	Q925s4 mus musculus
13	95.5	10.6	183	11 Q9WVP8	Q9wvp8 rattus norv
14	94	10.4	178	6 Q9TSJ4	Q9tsj4 oryctolagus
15	92.5	10.2	131	11 Q9ERK7	Q9erk7 peromyscus
16	90.5	10.0	103	11 Q88646	Q88646 marmota mon

17	90.5	10.0	178	6 Q9TVD3	Q9tvd3 oryctolagus
18	90.5	10.0	178	6 Q865X4	Q865x4 lama glama
19	88	9.7	170	12 Q91MZ9	Q91mz9 lumpy skin
20	87.5	9.7	130	11 Q70327	Q70327 mesocricetu
21	86.5	9.6	754	16 Q922C3	Q922c3 streptococc
22	86.5	9.6	754	16 Q8F0K7	Q8f0k7 streptococc
23	86.5	9.6	754	16 Q8K752	Q8k752 streptococc
24	85.5	9.5	189	12 Q80G59	Q80g59 bovine papu
25	85.5	9.5	601	16 Q8ZIG5	Q8zig5 versinia pe
26	85	9.4	141	10 Q40849	Q40849 picea glauc
27	83.5	9.2	324	2 Q83Z76	Q83z76 citrobacter
28	83.5	9.2	437	9 Q9AZM2	Q9azm2 bacterioph
29	83.5	9.2	437	16 Q9C194	Q9c194 lactococcus
30	82.5	9.1	961	11 Q80W87	Q80w87 rattus norv
31	82	9.1	463	11 Q8BLA4	Q8bla4 mus musculu
32	82	9.1	934	11 Q8C0U7	Q8c0u7 mus musculu
33	82	9.1	2184	12 Q8DX21	Q8dx21 canine dist
34	82	9.1	2184	12 P87575	P87575 canine dist
35	82	9.1	2752	5 Q9BUY0	Q9byu0 plasmodium
36	81.5	9.0	122	6 Q95LE3	Q95le3 canis famil
37	81.5	9.0	758	16 Q8DT31	Q8dt31 streptococc
38	80.5	8.9	275	5 Q8IIV0	Q8iiv0 plasmodium
39	80.5	8.9	932	5 O15924	O15924 dictyosteli
40	79.5	8.8	160	11 Q923T1	Q923t1 sigmodon hi
41	79.5	8.8	186	12 O11386	O11386 orf virus (
42	79.5	8.8	186	12 O11387	O11387 orf virus (
43	79.5	8.8	186	12 Q80G31	Q80g31 orf virus.
44	79.5	8.8	188	16 Q81CW3	Q81cw3 bacillus ce
45	79.5	8.8	319	16 Q92H29	Q92h29 rickettsia

ALIGNMENTS

RESULT 1

Q7SX60 PRELIMINARY; PRT; 175 AA.
AC Q7SX60
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Interleukin-20.
GN IL20.
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpho; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]_TaxID=99883;
RP SEQUENCE FROM N.A.
RA Lutfalla G., Roest Crolius H., Stange-Thomann N., Jaillon O.,
RA Mogens K., Monneron D.;
RT "Independent expansion of a lineage-specific gene family in
RT vertebrates: The class II cytokine receptors and their ligands in
RT mammals and fish.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY294557; AAP57414.1; -.
DR EMBL; AY294558; AAP57416.1; -.
SQ SEQUENCE 175 AA; 19838 MW; D86FA67E0038E034 CRC64;

Query Match 12.9%; Score 116.5; DB 13; Length 175;
Best Local Similarity 24.9%; Pred. No. 0.0013;
Matches 43; Conservative 30; Mismatches 85; Indels 15; Gaps 7;

QY 13 MGTIATSCILLALLV---QCGAARPTSSHCRLDKSNFQOPIYINRTPLAKASLADNN 69
Db 1 MKTIPSICLLFLAUCCTEBAQSQTLLVDSCSI-SADLQEMHQHNSIRL--NAITEDEE 57
QY 70 TDVRLIGEKLFGHVSMSERCYLMKQNFLEEVY-----FQSDRFPQPMQEVVFFIA 123
Db 58 IGKLLSKRLMEDVQDQRCRCFLVLQVFDKVPFSLSPHPQSSSSSLANTFIIV 117

QY 124 RISNRLSTCHIEGDDHLOQNVOKLDTWKIGES-GRKATGELDLFMSLR 175
 Db 118 R-KQMIQKCHCEQ-ETQKKVDSLDFAFKLEASNAVLKAVGELDTVLQWLQ 168

RESULT 2

Q802T4 PRELIMINARY; PRT; 183 AA.
 AC Q802T4;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Interleukin 10 homologue precursor.
 GN IL10.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM M.A.
 RA Zou J., Clark M.S., Seemans C.J.;
 RT "Characterisation, expression and promoter analysis of an interleukin
 10 homologue in the puffer fish, Fugu rubripes."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ539537; CAD62446.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; P:cytokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PRINTS; PR01294; INTRLEUKIN10.
 DR PRODOM; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 KW Signal.
 FT SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 183 AA; 21076 MW; 5DCF5667E8F6B404 CRC64;

Query Match 12.3%; Score 111.5; DB 13; Length 183;
 Best Local Similarity 22.6%; Pred. No. 0.0044;
 Matches 40; Conservative 33; Mismatches 73; Indels 31; Gaps 5;
 QY 19 SCILLALLVQGGAAPISSHC-----RLDKSNFQPPVITNRTFMLAKASLAD 67
 Db 8 SVLLLLCCACTVWCALCNKCCSFVEGPPARLKLRENVSQ-----IRDYEAN 57
 QY 68 NNTDVLLEKLFHGVSMSERCVLMKQVLFNFTLEVL-----PFQSDRFQPMQEWVP 120
 Db 58 DLDLIVLLDQSLVDITFTPTFACHMDGILRFYLDLSVLPALATVTAETRNKLDHVESIQ 117
 QY 121 FIARISNRLSTC-H-EGDDHLOQNVOKLDTWKIGESGEIKAIKAGELDLFMSLR 176
 Db 118 IFDQLKIEVNCXHFACNRRPDIV--LNSITFTEMDKGLYKANGELDLFNYIEN 172

RESULT 3

Q80WES PRELIMINARY; PRT; 178 AA.
 AC Q80WES;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DE Interleukin-10.
 GN IL10.
 OS Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 OX NCBI_TaxID=10042;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carruthers T., Herbst M.M., Schountz T.;

"Genomic organization of the deer mouse interleukin-10 gene."
 Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY251293; AAP13853.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; P:cytokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PRINTS; PR01294; INTRLEUKIN10.
 DR PRODOM; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 SQ SEQUENCE 178 AA; 20504 MW; 270064C1A7E8C1FC CRC64;

Query Match 11.8%; Score 106.5; DB 11; Length 178;
 Best Local Similarity 24.1%; Pred. No. 0.014;
 Matches 45; Conservative 34; Mismatches 69; Indels 39; Gaps 8;

QY 14 GTLATSCILLALLVQGGAA-----PISSHCRLD--KSNFQPPVITNRTFM 58
 Db 3 GSAPLCCILLALA---EVGASRGHNTQEGNCTHFPVSQTYTLRELRAAFDQV---KTFP 55
 QY 59 LAKEASLADNNTDVRLEKLFHGVSMSERCVLMKQVLFNFTLEVLFPQSDRFQPMQEV 118
 Db 56 QKXD-----OLDSILLTDSLMKDFKGYLGQALSEMTQFYLVFVM--PQAEHNGPEIKEH 108
 QY 119 VPFIAR-----ISNRLSTCHIEGDDHLOQNVOKLDTWKIGESGEIKAIKAGELDL 170
 Db 109 LNPLGKLTURRLQRFLPCENSKAVEQVSKDPNKLQENGIVYKAMSEFIFINCI 168
 QY 171 --FMSLR 175
 Db 169 EAYMTIIR 175

RESULT 4

Q7SX82 PRELIMINARY; PRT; 181 AA.
 AC Q7SX82;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE Interleukin-24.
 GN IL24.
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lutfalla G., Roest Crolius H., Stange-Thomann N., Jaillon O.,
 RA Mogense K., Monneron D.;
 RT "Independent expansion of a lineage-specific gene family in
 vertebrates: The class II cytokine receptors and their ligands in
 mammals and fish."
 RT mammals and fish."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY294559; AAP57417.1; -.
 DR EMBL; AY294560; AAP57418.1; -.
 SQ SEQUENCE 181 AA; 20610 MW; 0EC5AED39A6EBFD3 CRC64;

Query Match 11.7%; Score 106; DB 13; Length 181;
 Best Local Similarity 26.8%; Pred. No. 0.016;
 Matches 45; Conservative 30; Mismatches 73; Indels 20; Gaps 7;

QY 21 LLLALLVQGGAAPISSHCRLDKSNFQPPVITNRTFM-----LAKEASLADNNTDVRLEK 76
 Db 16 LLAVSLLIGWSLAPV----HLPHKALSPDLDDQTHKAVERVANQAQLEQDDPSRLMP 71
 QY 77 EKLFIH---GVSMSERCVLMKQVLFNFTLEVLFPQSDRFQPMQEVVPTIARISNRLST-- 131
 Db 72 ----HPPAGPDMLKLCCLHANLDFYLLNLSHSTDNQ--HTTRLRSLDLSRISHDLKAG 126

```

QY 132 CHIEGDDLHIQRNVOKLQDTVKKIGESGEIKALGELDLMPLRNACI 179
DB 127 CNI--TRYHDHQAHVQRQRYFEHQGHRRRTKALGEVDHILFYLDYCV 172

RESULT 5
Q8UJZ6
AC Q8UJZ6 PRELIMINARY; PRT; 177 AA.
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE BCRF1.
CS Cercopithecine herpesvirus 15.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=104228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RX MEDLINE=97048062; PubMed=8992903;
RA Franken M., Devergne O., Rosenzweig M., Annis B., Wang F.;
RT "Comparative analysis identifies conserved tumor necrosis factor
RT receptor-associated factor 3 binding sites in the human and simian
RT Epstein-Barr virus oncogene LMP1.";
RL J. Virol. 70:7819-7826(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RX MEDLINE=99412410; PubMed=10482645;
RA Rivallier P., Quirk C., Wang F.;
RT "Strong selective pressure for evolution of an Epstein-Barr virus
RT LMP2B homologue in the rhesus lymphocryptovirus.";
RL J. Virol. 73:8867-8872(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RX MEDLINE=20304984; PubMed=10846073;
RA Jiang H., Cho Y.-G., Wang F.;
RT "Structural, functional, and genetic comparisons of Epstein-Barr virus
RT nuclear antigen 3A, 3B, and 3C homologues encoded by the rhesus
RT lymphocryptovirus.";
RL J. Virol. 74:5921-5932(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RX MEDLINE=20440633; PubMed=10970361;
RA Rao P., Jiang H., Wang F.;
RT "Cloning of the rhesus lymphocryptovirus viral capsid antigen and
RT Epstein-Barr virus-encoded small RNA homologues and use in diagnosis
RT of acute and persistent infections.";
RL J. Clin. Microbiol. 38:3219-3225(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RX MEDLINE=21602573; PubMed=11739708;
RA Rivallier P., Jiang H., Cho Y.-G., Quink C., Wang F.;
RT "Complete Nucleotide Sequence of the Rhesus Lymphocryptovirus: Genetic
RT Validation for an Epstein-Barr Virus Animal Model.";
RL J. Virol. 76:421-426(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RA Moghaddam A., Koch J., Annis B., Wang F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RA Moghaddam A., Annis B., Wang F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=LCL8664;
RA Rivallier P., Quink C., Wang F.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RA Jiang H., Wang F.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RA Rao P.V., Jiang H., Wang F.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL8664;
RA Rivallier P., Jiang H., Cho Y.-G., Quink C., Wang F.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037858; AAK95412.1; -.
DR HSSP; P22301; 2ILK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
SQ SEQUENCE 177 AA; 20545 MW; 5F94050532E63A36 CRC64;

Query Match 11.5%; Score 104; DB 12; Length 177;
Best Local Similarity 24.6%; Pred. No. 0.024;
Matches 41; Conservative 30; Mismatches 80; Indels 16; Gaps 5;

QY 12 LMGTLATSLILLALLVQ---GGAAAPISSHCRDLK--SNFOOPYITNRTFMLEKASLA 66
DB 3 LRSGLTQLQCLVILQCLVMLYLAPACKGVSCNGLPMLRLDLDAFSRVKTFQMKD--- 58
QY 67 DNNTDVRILGKLFHGVSMSERCYLMKOVLANFTLEEVLPQSDRFQPYQEVVFFIAR-- 124
DB 59 --QLDNILLKESLLEDFKYGILGCQALSEMIQFYLEEVM--PQENQDPHAKHVNLSGENL 115
QY 125 --ISNRLSTCHIEGDDLHIQRNVOKLQDTVKKIGESGEIKALGELD 169
DB 116 KTLRLRLRRCHFLPCENKSKAVEQVNAFSKLQKGVKAMSEFDI 162

RESULT 6
Q9Q5L1
ID Q9Q5L1 PRELIMINARY; PRT; 171 AA.
AC Q9Q5L1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE VIL10.
OS Herpesvirus papio.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Baboon lymphocryptovirus BA65;
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.;
RA Hayward G.S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200364; AAF23949.1; -.
DR HSSP; P22301; 1INR.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.

```



```

Matches 42; Conservative 28; Mismatches 68; Indels 37; Gaps 8;
Qy 20 CLILLALL---VQGAAPAPI-SSHCRLDKSNFQPYTNRTFMLEAKESLASLADNNTDVLRI 75
Db 10 CLSILLLLNQQVPLEGQEFSSGQV--TGVLPELWEAFWTVKNTVQTQDDITSRL 67
Qy 76 GKKLFHGVSMSERCYLMKQVLFLEVLFPQSDRFQYMOEVVFFIARISNRLSTCHIE 135
Db 68 KPQVLRNVSGAESCYLAHSLKFLYNTV-----FKNYSKIAKF--KVLRST--LA 116
Qy 136 GDDLHIQRNVQKLD-TVKKIGESGE-----IXAIGELDIL 170
Db 117 NNFTIVMSQLQSKXSNMLPISAHQRFLLFRRAFKQLTEFVNLVKAFFGEVDIL 171

RESULT 13
Q9WVP8
ID Q9WVP8 PRELIMINARY; PRT; 183 AA.
AC Q9WVP8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DZ C49a.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP STRAIN=Sprague-Dawley;
RC MEDLINE=99308986; PubMed=10381256;
RA Soc C.; Shaw W.M.; Freymiller E.; Longaker M.T.; Bertolami C.N.;
RA Chiu R.; Tieu K.; Ting K.;
RT "Cutaneous rat wounds express c49a, a novel gene with homology to the
RT human melanoma differentiation associated gene, mda-7."
RL J. Cell. Biochem. 74:1-10 (1999).
DR EMBL; AF004774; AAB69171.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
SQ SEQUENCE 183 AA; 21052 MW; PF69A96AFC473B4F CRC64;

Query Match 10.68; Score 95.5; DB 11; Length 183;
Best Local Similarity 26.98; Pred. No. 0.18;
Matches 35; Conservative 19; Mismatches 45; Indels 31; Gaps 5;
Qy 67 DNNTDVLRIKGLFHGVSMSERCYLMKQVLFLEVLFPQSDRFQYMOEVVFFIARIS 126
Db 61 DELTSARLLKPVQLQNVSDAESCYLAHSLKFLYNTV-----FKNYSKIAKF--KVL 111
Qy 127 NRLSTCHIEGDDLHIQRNVQKLD-----TVKKIG-ESGIIKAIGE 166
Db 112 KSFT--LANNFIVMSKLOPSKDNAMLPISDSARRRFLFHRTFKQLDIEVALAKAFGE 169
Qy 167 LDLEFMSLRN 176
Db 170 VDIILLAWQN 179

RESULT 14
Q9TSJ4
ID Q9TSJ4 PRELIMINARY; PRT; 178 AA.
AC Q9TSJ4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Interleukin-10.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

```

```

OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Perkins H.D.; van Leeuwen B.H.; Hardy C.M.; Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565 (2000).
DR EMBL; AF068058; AAC23839.1; -.
DR HSSP; P22301; LINR.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
SQ SEQUENCE 178 AA; 20146 MW; A5E0B2A8F04D5170 CRC64;

Query Match 10.48; Score 94; DB 6; Length 178;
Best Local Similarity 22.08; Pred. No. 0.24;
Matches 37; Conservative 30; Mismatches 77; Indels 24; Gaps 4;
Qy 19 SCILLALLVOGGAAPISSHCRLDKSNFQOP-----YTNRFTMLEAKESL 65
Db 3 SSALLCLLVFLGGTGASRGQDTPAENSCHIFPGGLPHMLRELAARFGRVKTFFQSKD--- 59
Qy 66 ADNNTDVLRIKGLFHGVSMSERCYLMKQVLFLEVLFPQSDRFQYMOEVVFFIAR- 124
Db 60 ---QLNSMLTSLLELLEKVLGQALSEMIFQVTKQVM-PAENHSPAIREHVNLSIGEN 115
Qy 125 ---ISNRLSTCHIEGDDLHIQRNVQKLDITVKKIGESGEIKAIIGELDIL 169
Db 116 LKTLRLRLRQCHRFPLPCENSKSAVEQVKSFAFKLQEGSVYKAMSEEDI 163

RESULT 15
Q9ERG7
ID Q9ERG7 PRELIMINARY; PRT; 131 AA.
AC Q9ERG7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Interleukin-10 (fragment).
GN IL10.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Herbst M.M.; Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
RT necrosis factor genes.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307012; AAG30263.1; -.
DR HSSP; P22301; LINR.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
FT NON_TER 1 1
FT NON_TER 131 131

```


SQ SEQUENCE 131 AA; 15398 MW; 6EAGEA20CDC0234F CRC64;
Query Watch 10.2%; Score 92.5; DB 11; Length 131;
Best Local Similarity 24.4%; Pred. No. 0.23;
Matches 29; Conservative 25; Mismatches 54; Indels 11; Gaps 3;
QY 55 RTFMLAKEASLADNNTDVLIGKLFHGVSMGRCVYMKQVLNFTLEEVLPQSDRFQPY 114
Db 19 KTFQKQD-----QLDSILLTDSLKDKFKGVLGCOALSEMIQFYLVVW-FOAENHGPE 71
QY 115 MOEVPFETAR-----SNRLSTCHIEGDDLHIQNVOKLKDITYKKIGESGEIKAI GELD 169
Eb 72 IKEHNFELGKLTLLRRRLQRCRFLPCENKSKAVEQVKSDFENKLENGVYKAMSEFDI 130

Search completed: June 30, 2004, 19:36:04
Cob time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:27:38 ; Search time 23 Seconds
(without alignments)
401.785 Million cell updates/sec

Title: US-10-050-552A-2
Perfect score: 903
Sequence: 1 MAALQKSVSSFLMGTLATSC.....EIKAGELDLFLFMSLRNACI 179

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/2/iaa/5A.COMB.pap.*
2: /cgm2_6/ptodata/2/iaa/5B.COMB.pap.*
3: /cgm2_6/ptodata/2/iaa/6A.COMB.pap.*
4: /cgm2_6/ptodata/2/iaa/6B.COMB.pap.*
5: /cgm2_6/ptodata/2/iaa/PCTUS.COMB.pap.*
6: /cgm2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	897	99.3	179	4	US-09-870-574-2
2	875	96.9	179	4	US-09-419-568F-28
3	875	96.9	179	4	US-09-354-243B-28
4	718	79.5	179	3	US-09-178-973B-15
5	718	79.5	179	4	US-09-419-568F-27
6	718	79.5	179	4	US-09-354-243B-27
7	714	79.1	179	3	US-09-178-973B-16
8	103	11.4	170	1	US-08-270-805C-2
9	103	11.4	170	2	US-08-410-654B-2
10	103	11.4	170	2	US-08-474-851-2
11	103	11.4	170	2	US-08-481-560-2
12	103	11.4	170	2	US-08-934-959-4
13	103	11.4	170	3	US-08-170-113-2
14	103	11.4	170	3	US-08-765-094C-26
15	103	11.4	170	3	US-09-082-797-26
16	103	11.4	170	3	US-08-643-810A-2
17	103	11.4	170	4	US-09-552-613-2
18	103	11.4	170	4	US-09-512-256-26
19	98.5	10.9	154	4	US-09-452-624A-3
20	97.5	10.8	220	3	US-08-884-077-2
21	96.5	10.7	178	1	US-08-270-805C-1
22	96.5	10.7	178	2	US-08-410-654B-1
23	96.5	10.7	178	2	US-08-474-851-1
24	96.5	10.7	178	2	US-08-481-560-1
25	96.5	10.7	178	2	US-08-934-959-6
26	96.5	10.7	178	3	US-08-170-113-1
27	96.5	10.7	178	3	US-08-765-094C-25

```

28 96.5 10.7 178 3 US-09-082-797-25 Sequence 25, Appl
29 96.5 10.7 178 3 US-08-643-810A-1 Sequence 1, Appl
30 96.5 10.7 178 4 US-09-552-613-1 Sequence 1, Appl
31 96.5 10.7 178 4 US-09-512-256-25 Sequence 25, Appl
32 96.5 10.7 178 4 US-09-462-941-16 Sequence 16, Appl
33 92.5 10.2 147 1 US-08-270-805C-4 Sequence 4, Appl
34 92.5 10.2 147 2 US-08-410-654B-4 Sequence 4, Appl
35 92.5 10.2 147 2 US-08-474-851-4 Sequence 4, Appl
36 92.5 10.2 147 2 US-08-481-560-4 Sequence 4, Appl
37 92.5 10.2 147 3 US-08-170-113-4 Sequence 4, Appl
38 92.5 10.2 147 3 US-08-643-810A-4 Sequence 4, Appl
39 92.5 10.2 147 4 US-09-552-613-4 Sequence 4, Appl
40 92.5 10.2 147 5 PCT-US93-07646-2 Sequence 2, Appl
41 92.5 10.2 166 4 US-09-452-624A-4 Sequence 4, Appl
42 91.5 10.1 160 1 US-08-270-805C-3 Sequence 3, Appl
43 91.5 10.1 160 2 US-08-410-654B-3 Sequence 3, Appl
44 91.5 10.1 160 2 US-08-474-851-3 Sequence 3, Appl
45 91.5 10.1 160 2 US-08-481-560-3 Sequence 3, Appl

```

ALIGNMENTS

```

RESULT 1
US-09-870-574-2
; Sequence 2, Application US/09870574
; Patent No. 6551799
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin L.
; APPLICANT: Aggarwal, Sudepta
; APPLICANT: Xie, Ming-Hong
; APPLICANT: Maruoka, Ellen M.
; APPLICANT: Foster, Jessica S.
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
; THE SAME AND METHODS FOR THE TREATMENT OF PANCREATIC DISORDER
; FILE REFERENCE: P2806-I (US)
; CURRENT APPLICATION NUMBER: US/09/870,574
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/169,495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-870-574-2

```

```

Query Match          99.3%; Score 897; DB 4; Length 179;
Best Local Similarity 98.3%; Pred. No. 2.2e-100; Indels 0; Gaps 0;
Matches 176; Conservative 3; Mismatches 0;
QY 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISCHRLDKSNFQOPIYTNRTFMLA 60
   |||||
Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISCHRLDKSNFQOPIYTNRTFMLA 60
   |||||
QY 61 KEASLADNNTDVRLLGKLFHGVSMSERCYLMKQVNLFTLSEVLFPQSDRFPQYMQEVPV 120
   |||||
Db 61 KEASLADNNTDVRLLGKLFHGVSMSERCYLMKQVNLFTLSEVLFPQSDRFPQYMQEVPV 120
   |||||
QY 121 FIARISNRLSTCHIEGDDLHQRNQQKLDVTKVKGESGEIKAGELDLFLFMSLRNACI 179
   |||||
Db 121 FIARISNRLSTCHIEGDDLHQRNQQKLDVTKVKGESGEIKAGELDLFLFMSLRNACI 179
   |||||

```

```

RESULT 2
US-09-419-568F-28
; Sequence 28, Application US/09419569F

```

[illegible]

QY 1 MAALQKSVSFLMGTLATSCILLALIVQGGAAAPISCHCLDKSNFQOPYITNRTFMLA 60
Db 1 MAVLQKSMSPFLMGTLAASCLLLIALWAQANALPVTNCRCKLEVSNFQOPYIVNRTEFMA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEVLFPQSDRFPQYQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEVLFPQSDRFPQYQEVVP 120
QY 121 FIARISNRLSTCHIETGDDLHIQRNVOKLDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179
Db 121 FLTKLSNQLSSCHISGDDQNIQKNVRLKETVKKIGESGEIKAI GELDLFLFMSLRNACV 179

RESULT 6
US-09-354-243B-27
; Sequence 27, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
; TITLE OF INVENTION: (TIPS)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 27
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
US-09-354-243B-27

Query Match 79.5%; Score 718; DB 4; Length 179;
Best Local Similarity 76.5%; Pred. No. 9.5e-73;
Matches 137; Conservative 22; Mismatches 20; Indels 7 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCILLALIVQGGAAAPISCHCLDKSNFQOPYITNRTFMLA 60
Db 1 MAVLQKSMSPFLMGTLAASCLLLIALWAQANALPVTNCRCKLEVSNFQOPYIVNRTEFMA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEVLFPQSDRFPQYQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEVLFPQSDRFPQYQEVVP 120
QY 121 FIARISNRLSTCHIETGDDLHIQRNVOKLDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179
Db 121 FLTKLSNQLSSCHISGDDQNIQKNVRLKETVKKIGESGEIKAI GELDLFLFMSLRNACV 179

RESULT 7
US-09-178-973B-16
; Sequence 16, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
; TITLE OF INVENTION: (TIPS)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543
; CURRENT APPLICATION NUMBER: US/09/178,973B
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 179
; TYPE: PRT

; ORGANISM: Mus musculus
US-09-178-973B-16
Query Match 79.1%; Score 714; DB 3; Length 179;
Best Local Similarity 76.0%; Pred. No. 2.9e-78;
Matches 136; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCILLALIVQGGAAAPISCHCLDKSNFQOPYITNRTFMLA 60
Db 1 MAVLQKSMSPFLMGTLAASCLLLIALWAQANALPVTNCRCKLEVSNFQOPYIVNRTEFMA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEVLFPQSDRFPQYQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEVLFPQSDRFPQYQEVVP 120
QY 121 FIARISNRLSTCHIETGDDLHIQRNVOKLDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179
Db 121 FLTKLSNQLSSCHISGDDQNIQKNVRLKETVKKIGESGEIKAI GELDLFLFMSLRNACV 179

RESULT 8
US-08-270-805C-2
; Sequence 2, Application US/08270805C
; Patent No. 5776451
; GENERAL INFORMATION:
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Kevin K. Moore
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of Interleukin10 in Adoptive Immunotherapy
; TITLE OF INVENTION: of Cancer
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,805C
FILING DATE: 05-July-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,564
FILING DATE: 23-Dec-1992
APPLICATION NUMBER: US 07/830,493
FILING DATE: 04-Feb-1992
APPLICATION NUMBER: US 07/641,342
FILING DATE: 16-Jan-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0142Q2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-270-805C-2

Query Match 11.4%; Score 103; DB 1; Length 170;
Best Local Similarity 24.8%; Pred. No. 0.0002;
Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;

57	LLKESILLEDFKYLGCCALSEMIQFYLEEV-POAENQDPEAKDHNVLNGENLKLRLR	115
129	LSTCHTEGGDLHQRNVQKLDTKVKIGESCEIKAGELDL	169
116	LRCHRFPLPCENSKAVEQIKNAFNKLGQKRGYYAMGEFDI	156

```

1 RESULT 10
2 US-08-474-851-2
3 ; Sequence 2, Application US/08474851
4 ; Patent No. 5837232
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Rene de Waal Malefyt
9 ;
10 ; APPLICANT: Di-Hwei Hsu
11 ;
12 ; APPLICANT: Anne O'Garra
13 ;
14 ; APPLICANT: Hergen Spits
15 ;
16 ; TITLE OF INVENTION: Use of An Interleukin
17 ;
18 ; TITLE OF INVENTION: A B Cell Mediated Auto
19 ;
20 ; NUMBER OF SEQUENCES: 61
21 ;
22 ; CORRESPONDENCE ADDRESS:
23 ;
24 ; ADDRESSEE: Schering-plough Corporation
25 ;
26 ; STREET: 2000 Galloping Hill Road
27 ;
28 ; CITY: Kenilworth
29 ;
30 ; STATE: New Jersey
31 ;
32 ; COUNTRY: USA
33 ;
34 ; ZIP: 07033
35 ;

```

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,851
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/410,654
 FILING DATE: 24-MAR-1995
 APPLICATION NUMBER: US 08/229,854
 FILING DATE: 19-APR-1994
 APPLICATION NUMBER: US 07/926,853
 FILING DATE: 06-AUG-1992
 APPLICATION NUMBER: US 07/742,129
 FILING DATE: 06-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Foulke, Cynthia L.
 REGISTRATION NUMBER: 32,364
 REFERENCE/DOCKET NUMBER: DX0221KQIGD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-298-2987
 TELEFAX: 908-298-5388
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-474-851-2

	Query Match	11.4%	Score 103;	DB 2;	Length 170;	
	Best Local Similarity	24.8%;	Pred. No. 0.0002;			
	Matches	40;	Conservative	27;	Mismatches	68; Indels 26; Gaps 6
Qy	20	CLLLALLVGGAAAPISSHCRDKSNPQQ-----PYINRTTMLAKBASLADNNTIV	72			
		: : :				
Dd	11	CLVLVLYLAPECGG---TDQC---DNFPQMLRLDLDAFSAVKTFEFTQND-----EVDN	56			
		: : :				
Qy	73	RLIGEKILFHGVSMSERCYLMKQVINFTLEVLFPQSDRFPQPMQEWVFPIAR-----ISNR	128			
		: : :				
Dd	57	LILKESILEDPKGYLGCOALSEMIFDYLEYVM--POARNQDPRAKHDSVNSLGENLKTLRLR	115			
		: : :				

Db 116 LRRCHFLPCENKSKAVEQIKNAFNKLEKGIYKAMSEFDI 156

RESULT 12

US-08-934-959-4

Sequence 4, Application US/08934959

Patent No. 5989867

GENERAL INFORMATION:

APPLICANT: Knappe, Andrea

APPLICANT: Fickenscher, Helmut

APPLICANT: Fleckenstein, Bernhard

TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,959

FILING DATE: 22-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/027,368

FILING DATE: 23-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0644X

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-852-9196

TELEFAX: 650-496-1200

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-934-959-4

Query Match 11.4%; Score 103; DB 2; Length 170;

Best Local Similarity 24.8%; Pred. No. 0.0002;

Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;

QY 20 CILLALLVQGGAAAPISHSCHLDSNFOQ-----PYITRTFMKEASLADNTDV 72

Db 11 CULVLYLAPECGG----TDQC-----DNPPQMLRLDFAFRVKTFFQTKD-----EVDN 56

QY 73 RLIGEKLFHGVSMSERCYLMKQVLTLEEVLPQSDRFPQYMQEVVPIAR-----ISNR 128

Db 57 LLLKESLLEDFKGYLGCOALSEMIQFYLEEVN-POAENQDPEAKDHNLSLGENLKLRLR 115

QY 129 LSTCHIEGDDLHIQRNVQKLDTVKKIGESGEIKAGELDL 169

Db 116 LRRCHFLPCENKSKAVEQIKNAFNKLEKGIYKAMSEFDI 156

RESULT 13

US-08-170-113-2

Sequence 2, Application US/08170113

Patent No. 6106823

GENERAL INFORMATION:

APPLICANT: Vieira, Paulo J.

APPLICANT: Moore, Kevin W.

APPLICANT: de Waal Malefyt, Rene

; APPLICANT: de Vries, Jan E.
; APPLICANT: Fluckinger, Anne-Catherine
; APPLICANT: Banctereau, Jacques
; TITLE OF INVENTION: TREATMENT OF NEOPLASTIC DISEASE WITH
; TITLE OF INVENTION: INTERLEUKIN-10
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1124
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,113
; FILING DATE: 17-DEC-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,419
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/091,333
; FILING DATE: 12-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/020,018
; FILING DATE: 17-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/830,496
; FILING DATE: 04-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,347
; FILING DATE: 16-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0116QLKX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-170-113-2

Query Match 11.4%; Score 103; DB 3; Length 170;
Best Local Similarity 24.8%; Pred. No. 0.0002;
Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 5;
QY 20 CLLLALLVGGGAAPISSHCRDKSNFQ-----PYITNRTFMLAKEASLADNNTDV 72
Db 11 CLVLLYLAPEGCG-----TDQC-----DNFPQMLRDLRDAFSEVKTFFQTKD-----EVDN 56
QY 73 RLIGEKLFGVSWNSERCYLMKVNLFTLEEVLPQSDRFQPMQEVVPPFIAR-----ISNR 128
Db 57 LLKESLLEDFKGYLGQALSEMIQFYLEEVMPQAEHQDPEAKDHVNSLGENLKLRLR 115
QY 129 LSTCHIEGDDLHIQRNVOKLDTVKKIGESGEIKAI GELD 169
Db 116 LRCHRLPCENSKS KAVEQIKNAFNKLGKGIYKAMSEFDI 156

RESULT 14
US-08-765-094C-26
; Sequence 26, Application US/08765094C

; Patent No. 6159937
; GENERAL INFORMATION:
; APPLICANT: GRONHOJ LARSEN, Christian
; APPLICANT: GESSER, Borbala
; TITLE OF INVENTION: IMMUNOMODULATORS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,094C
; FILING DATE: 06-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK95/00227
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0800/94
; FILING DATE: 05-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: GRONHOJ-LARSEN-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)628-5197
; TELEFAX: (202)737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-765-094C-26

Query Match 11.4%; Score 103; DB 3; Length 170;
Best Local Similarity 24.8%; Pred. No. 0.0002;
Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;
QY 20 CLLLALLVGGGAAPISSHCRDKSNFQ-----PYITNRTFMLAKEASLADNNTDV 72
Db 11 CLVLLYLAPEGCG-----TDQC-----DNFPQMLRDLRDAFSEVKTFFQTKD-----EVDN 56
QY 73 RLIGEKLFGVSWNSERCYLMKVNLFTLEEVLPQSDRFQPMQEVVPPFIAR-----ISNR 128
Db 57 LLKESLLEDFKGYLGQALSEMIQFYLEEVMPQAEHQDPEAKDHVNSLGENLKLRLR 115
QY 129 LSTCHIEGDDLHIQRNVOKLDTVKKIGESGEIKAI GELD 169
Db 116 LRCHRLPCENSKS KAVEQIKNAFNKLGKGIYKAMSEFDI 156

RESULT 15
US-09-082-797-26
; Sequence 26, Application US/09082797
; Patent No. 6168791
; GENERAL INFORMATION:
; APPLICANT: GRONHOJ LARSEN, Christian
; APPLICANT: GESSER, Borbala
; TITLE OF INVENTION: IMMUNOMODULATORS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Suite 300
; CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,797
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,094
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0800/94
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: GRONHOJ-LARSEN=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-082-797-26

Query Match 11.4%; Score 103; DB 3; Length 170;
Best Local Similarity 24.8%; Ered. No. 0.0002;
Matches 40; Conservative 27; Mismatches 58; Indels 26; Gaps 6;
QY 20 CLLLALLVGGGAAAPISCHRLDKSNFQ-----PYITNTPMLAKEASLADNNTDV 72
DB 11 CLVLLYLAPECGG---TDQC---DNFPQMLRLDRDAFSRVKTFQTKD-----EVDN 56
QY 73 RLIGEXLFHCVSNSECYLMKQVNLFTLEVLFPQSDRFQPYMQEVVFFIAR----LSNR 128
DB 57 LLKESLEDFKYLGCQALSEMIQFYLEVM-PQENQDPKADHVNSIGENIKTLRL 115
QY 129 LSTCHIEGDDLHTRQNVQKLKDTVKKIGESGEIKAI GELD 169
DB 116 LRCHRFPCENKSKAVEQIKNAFNKIQEKGIYKANSEFDI 156

Search completed: June 30, 2004, 19:34:04
Job time : 24 secs

A;Cross-references: GB:M57627; NID:g186270; PIDN:AAA63207.1; PID:g186271
R;Mindor, W.T.; Syto, R.; Tzatzopoulos, A.; Zhang, R.; Durkin, J.; Baldwin, S.; Paliwal
Biochemistry 32, 8807-8815, 1993
A;Title: Disulfide bond assignments and secondary structure analysis of human and murine
A;Reference number: A48693; MUID:93372085; PMID:8364028
A;Contents: annotation; disulfide bonds in recombinant protein
R;Sanjanwala, B. The EMBL Data Library, October 1994
submitted to the EMBL Data Library, October 1994
A;Reference number: G07695
A;Accession: G01539
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-178 <SAN>
A;Cross-references: EMBL:U16720; NID:g1041812; PIDN:AAA80104.1; PID:g1041813
R;Kube, D.; Platzer, C.; von Knehten, A.; Straub, H.; Hafner, M.; Tesch, H.
submitted to the EMBL Data Library, March 1994
A;Description: Isolation of the human interleukin-10 promoter. Characterization of the P
A;Reference number: S49110
A;Accession: S49110
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6, 'PVAWSS' <KUB>
A;Cross-references: EMBL:X78437; NID:g1167492
R;Platzer, C.; Volk, H.D.; Platzer, M.
DNA Seq. 4, 399-401, 1994
A;Title: 5' noncoding sequence of human IL-10 gene obtained by oligo-cassette PCR walkin
A;Reference number: I37890; MUID:95143580; PMID:7841462
A;Accession: I37890
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <PLA>
A;Cross-references: EMBL:X73536; NID:g452395; PIDN:CAA51942.1; PID:g580177
C;Genetics:
A;Gene: GDB:IL10; IL-10
A;Cross-references: GDB:128636; OMIM:124092
A;Map position: 1q31-1q32
A;Introns: 55/3; 75/3; 126/3; 148/3
C;Superfamily: interleukin-10
C;Keywords: cytokine; glycoprotein; lymphokine; T-cell
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-178/Product: interleukin-10 #status predicted <MAT>
F;30-126,80-132/Disulfide bonds: #status experimental
F;134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.7%; Score 96.5; DB 2; Length 178;
Best Local Similarity 22.4%; Pred. No. 0.1;
Matches 41; Conservative 33; Mismatches 78; Indels 31; Gaps 6;
QY 18 TSCLLALLVQGGAAAP-----ISSHRLDKSN-----FOQFYTNRTFMLEKASL 65
DB 3 SSALLCCLVLLTGVRASPGQGTQSENCTHFGNLPNMLRDLRDAFSEVKTFQMKD--- 59
QY 66 ADNNTDVRLLGKELFHGVSMSERCYLMKQVNLFTLEVLFPQSDRFPQYVQVVPF 121
DB 60 ---QLDNLLKESLLDFKGYLGCQALSEMIQFYLEEVMPQAEHQDPDIKAHVNLSGEN 115
QY 122 IARISNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGEIKATGELDL-----LFMS 173
DB 116 LKTLRLRLRRCHRFPCENKSKAVEQVKNAPNKLQEKGIYKAMSEFDIFINYEAYMTK 175
QY 174 LRN 176
DB 176 LRN 178

RESULT 3
A34853
interleukin-10 precursor - mouse
N;Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
C;Species: Mus musculus (house mouse)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 26-Aug-1999
C;Accession: A34853; I56136
R;Moore, K.W.; Vieira, P.; Fiorentino, D.F.; Trounstein, M.L.; Khan, T.A.; Mosmann, T.R.

Science 248, 1230-1234, 1990
A;Title: Homology of cytokine synthesis inhibitory factor (IL-10) to the Epstein-Barr
A;Reference number: A34853; MUID:90273182; PMID:2161559
A;Accession: A34853
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <MOO>
A;Cross-references: GB:M37897; NID:g198288; PIDN:AAA39274.1; PID:g198289
R;Kim, J.M.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Khan, T.A.; Moore, K.W.
J. Immunol. 148, 3618-3623, 1992
A;Title: Structure of the mouse IL-10 gene and chromosomal localization of the mouse
A;Reference number: I56136; MUID:92268508; PMID:1350294
A;Accession: I56136
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-178 <RES>
A;Cross-references: GB:M84340; NID:g198291; PIDN:AAA39275.1; PID:g198292
C;Genetics:
A;Gene: IL10
A;Introns: 55/3; 75/3; 126/3; 148/3
C;Superfamily: interleukin-10
C;Keywords: cytokine; lymphokine; T-cell

Query Match 10.0%; Score 90.5; DB 2; Length 178;
Best Local Similarity 23.3%; Pred. No. 0.37;
Matches 40; Conservative 34; Mismatches 71; Indels 27; Gaps 8;
QY 14 GTTATSCLLALLVQGGAA-----PI-SSHRLD-KSNFOQPYTNRTFMLEAK 61
DB 3 GSALLCCLVLLTGVRISRGQYSREDNCTHFPVQGSMLLELRTAFSQV-----KTFQTK 58
QY 62 EASLADNNTDVRLLGKELFHGVSMSERCYLMKQVNLFTLEVLFPQSDRFPQYVQVVPF 121
DB 59 D-----QLDNILLTDSLMQDFKGYLGCQALSEMIQFYLEEVMPQAEKGGPEIKELHLS 111
QY 122 IAR-----ISNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGEIKATGELDL 169
DB 112 LGEKLTIRMLRRCHRFPCENKSKAVEQVKSDFNKLDQOQSVYKAMNEFI 163

RESULT 4
I46591
interleukin 10 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 26-Aug-1999
C;Accession: I46591
R;Blanco, G.; Gnanello, P.; Germana, S.; Baetscher, M.; Sachs, D.H.; LeGuern, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 2800-2804, 1995
A;Title: Molecular identification of porcine interleukin 10: regulation of expression
A;Reference number: I46591; MUID:95224028; PMID:7708727
A;Accession: I46591
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-175 <BLA>
A;Cross-references: GB:L20001; NID:g309792; PIDN:AAA74410.1; PID:g309793
C;Genetics:
A;Gene: IL-10
C;Superfamily: interleukin-10

Query Match 9.6%; Score 87; DB 2; Length 175;
Best Local Similarity 25.6%; Pred. No. 0.78;
Matches 43; Conservative 28; Mismatches 69; Indels 28; Gaps 8;
QY 19 SCLLALLVQGGAAAPISSHRLDKSNFOQPYTNRTFMLEKASLA-----D 67
DB 3 SSALLCCLVLLTGVRISRGQYSREDNCTHFPVQGSMLLELRTAFSQV-----KTFQTK 55
QY 68 NNTDVRLLGKEL--FHGVSMSERCYLMKQVNLFTLEVLFPQSDR----FQPYVQVVPF 121
DB 56 QMGDLTLTGSLLEDFKGYL---CCQALSEMIQFYLEEDVM-PKAESEDGEIKHVNLSGEK 111
QY 122 IARISNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGEIKATGELDL 169

[illegible]


```
Query Match      8.8%; Score 79.5; DB 2; Length 688;
Best Local Similarity 22.3%; Pred. No. 21;
Matches 42; Conservative 27; Mismatches 62; Indels 57; Gaps 8;

QY 17 ATSCILLALLVQGGAAAPIS--SHCRLDKSNFQPPYITNRTFMLAKEASL----- 65
DB 129 AASATLFLAHI-----APIKVSACRI--ARVDNEFIINPSASLLNQSSLDLFFVSGTKE 180

QY 66 ADNNTDVRLLIGKLI-----FHGVSMSERCYLMKQVNLFTLEEVLPQSDRF- 111
DB 181 SLNMIEMRSLGKLNALBEPMLALELAQKSLKETCALYEAEFTPYQNELLFKEGGIV 240

QY 112 -----QPYMQQVFFPIARISNRLSTCHIEGDDLHIQRWQKLTOTVTKIGSGEI 161
DB 241 LNERLLDLKNGVDFDEIIR-----GISSALSRENVN--FKEVAKKISEAHSE 286

QY 162 KALGELDOL 169
DB 287 FSLEEIEEL 294

RESULT 13
E64671
polynucleotide phosphorylase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 27-Oct-2003
C:Accession: E64671
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: E64671
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-688 <COM>
A:Cross-references: GB:AE000627; GB:AE000511; NID:g2314373; PIDN:AAD08258.1; PID:g231437
C:Superfamily: polynucleotide nucleotidyltransferase

Query Match      8.8%; Score 79.5; DB 2; Length 688;
Best Local Similarity 21.4%; Pred. No. 21;
Matches 39; Conservative 28; Mismatches 60; Indels 55; Gaps 7;

QY 17 ATSCILLALLVQGGAAAPIS--SHCRLDKSNFQPPYITNRTFMLAKEASL----- 65
DB 129 AASATLFLAHI-----APIKVSACRI--ARMDNEFIINPSASLLNQSSLDLFFVSGTKE 180

QY 66 ADNNTDVRLLIGKLI-----FHGVSMSERCYLMKQVNLFTLEEVLPQSDRF- 111
DB 181 SLNMIEMRSLGKLNALBEPMLALELAQKSLKETCALYEAEFTPYQNELLFKEGGIV 240

QY 112 -----QPYMQQVFFPIA-----RISNRLSTCHIEGDDLHIQRWQKLT 149
DB 241 FNERLLDLKNGVDFDEIIRGISSALSRENVNFTLEARKISEAHSEFSLEIELSLEKVK 300

QY 150 DT 151
DB 301 KT 302

RESULT 14
S50608
hypothetical protein YER105c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
C:Accession: S50608
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 9747, 8198, 9781, and lambda clones
A:Reference number: S50436

A:Accession: S50608
A:Molecule type: DNA
A:Residues: 1-1391 <DIE>
A:Cross-references: EMBL:U18839; NID:g603313; PIDN:AAB64660.1; PID:g603343; MIPS:YER1
C:Genetics:
A:Gene: SGD:NUP157
A:Cross-references: SGD:S0000907; MIPS:YER105C
A:Map position: 5R

Query Match      8.8%; Score 79.5; DB 2; Length 1391;
Best Local Similarity 23.7%; Pred. No. 48;
Matches 28; Conservative 25; Mismatches 48; Indels 17; Gaps 5;

QY 1 MAALQKSVSFLMGTATSCLLLLALLVQGGAAAPI-----SHCRLDKSNF---QOPYITN 54
DB 342 ISOLEVDQSGVGLHTLSTKSVIRSYLITSNGLVGPVLIDAAHTRRGNALGVKNPSPLSN 401

QY 55 RTEMLAK--EASLADNN---TOVRLIGKLIHGVSMSERCYLMKQVNLFTLEEVLP 106
DB 402 RAPRIAKIVSICMENDLFLAVITTTGVRLYPKGSISRR-----SIGSLKLDVSKPP 454

RESULT 15
S59996
AMP deaminase (EC 3.5.4.6) 2 isoform L - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
C:Accession: S59996
R:van den Bergh, F.; Sabina, R.L.
Biochem. J. 312, 401-410, 1995
A:Title: Characterization of human AMP deaminase 2 (AMPD2) gene expression reveals a
A:Reference number: S59994; MUID:96103174; PMID:8526848
A:Accession: S59996
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-605 <VAN>
A:Cross-references: EMBL:U16269; NID:g608496; PIDN:AAB06511.1; PID:g608497
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
C:Genetics:
A:Introns: 175/1; 222/2; 360/3; 404/3
C:Superfamily: AMP deaminase
C:Keywords: alternative splicing; hydrolase

Query Match      8.7%; Score 78.5; DB 2; Length 605;
Best Local Similarity 25.7%; Pred. No. 22;
Matches 38; Conservative 28; Mismatches 63; Indels 19; Gaps 8;

QY 22 LLALLVQGGAAAPISHC--RED--KSNFQPPYITNRTFMLEAKEASLADNN-TDVRLLIG 76
DB 242 VLMALING-----PIKSFYRRLQYLSKQFMHVLNEMKELAAQKVPHRDPYNIKVD 297

QY 77 EKLHGVSMSERCYL--MKQVNLFTLEEVLPQSDRFQPYMQVYVPPFIARISNRLSTCHI 134
DB 298 THIHSSCMNQKHLRFIKRMRHLEEVHVHVGQREQT--LREVFESMNLTAVDLS---V 353

QY 135 EGGDLHIQNV-----OKLKDVTVKIGES 158
DB 354 DTLDVHADRTFHRFDKFNKYNPIGES 381

Search completed: June 30, 2004, 19:33:29
Job time : 22 secs
```

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	903	100.0	179	13	US-10-050-552A-2	Sequence 1
2	903	100.0	179	15	US-10-238-965-2	Sequence 2
3	897	99.3	179	9	US-09-728-911-15	Sequence 1
4	897	99.3	179	9	US-09-870-574-2	Sequence 2
5	897	99.3	179	9	US-09-965-528-18	Sequence 1
6	897	99.3	179	10	US-09-925-055D-8	Sequence 8
7	897	99.3	179	10	US-09-746-375-2	Sequence 1
8	897	99.3	179	12	US-10-081-056-354	Sequence 3
9	897	99.3	179	12	US-10-219-535-244	Sequence 2
10	897	99.3	179	12	US-10-232-230-244	Sequence 2
11	897	99.3	179	12	US-09-969-984-18	Sequence 1
12	897	99.3	179	12	US-10-063-745-154	Sequence 1
13	897	99.3	179	12	US-10-063-512-154	Sequence 1
14	897	99.3	179	12	US-10-063-513-154	Sequence 1
15	897	99.3	179	12	US-10-063-515-154	Sequence 1

APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BURFORD, Neil
APPLICANT: BANDMAN, Olga
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda
APPLICANT: LU, Dyoung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: 92-0701 USA
CURRENT APPLICATION NUMBER: US/09/965,528
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/134,949
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/144,270
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: 60/146,700
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/157,508
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 179
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020187523A1 5571181CD1
US-09-965-528-18

Query Match 99.3%; Score 897; DB 9; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISSHCRDLKSNFQOPIYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISSHCRDLKSNFQOPIYITNRTFMLA 60
Qy 61 KEASLADNNTDVRLLIGEKLPHGVSMSERCYLMKQVNTLLEVLFPQSDRFQPMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLPHGVSMSERCYLMKQVNTLLEVLFPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDHLHQRNVQKLDVTVKKGESGEIKATGELDLFMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDHLHQRNVQKLDVTVKKGESGEIKATGELDLFMSLRNACI 179

RESULT 6
US-09-925-055D-8
Sequence 8, Application US/09925055D
Publication No. US20030157096A1
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne R.
APPLICANT: Topouzis, Stavros
TITLE OF INVENTION: SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-56
CURRENT APPLICATION NUMBER: US/09/925,055D
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/223,827
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US 60/250,876
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 179
TYPE: PRT
ORGANISM: homo sapiens
US-09-925-055D-8

Query Match 99.3%; Score 897; DB 10; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;

Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISSHCRDLKSNFQOPIYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISSHCRDLKSNFQOPIYITNRTFMLA 60
Qy 61 KEASLADNNTDVRLLIGEKLPHGVSMSERCYLMKQVNTLLEVLFPQSDRFQPMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLPHGVSMSERCYLMKQVNTLLEVLFPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDHLHQRNVQKLDVTVKKGESGEIKATGELDLFMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDHLHQRNVQKLDVTVKKGESGEIKATGELDLFMSLRNACI 179

RESULT 7

US-09-746-375-2
Sequence 2, Application US/09746375
Publication No. US20030170823A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Kindsvogel, Wayne
TITLE OF INVENTION: NOVEL CYTOKINE ZCYT018
FILE REFERENCE: 99-106
CURRENT APPLICATION NUMBER: US/09/746,375
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 60/172,105
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/***,***
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 179
TYPE: PRT
ORGANISM: Homo sapiens
US-09-746-375-2

Query Match 99.3%; Score 897; DB 10; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;

Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISSHCRDLKSNFQOPIYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISSHCRDLKSNFQOPIYITNRTFMLA 60
Qy 61 KEASLADNNTDVRLLIGEKLPHGVSMSERCYLMKQVNTLLEVLFPQSDRFQPMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLPHGVSMSERCYLMKQVNTLLEVLFPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDHLHQRNVQKLDVTVKKGESGEIKATGELDLFMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDHLHQRNVQKLDVTVKKGESGEIKATGELDLFMSLRNACI 179

RESULT 8

US-10-081-056-354
Sequence 354, Application US/10081056
Publication No. US20040043927A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerbet, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scott A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Stephan, Jean-Philippe P.
APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C1
CURRENT APPLICATION NUMBER: US/10/081,056
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: PCT/US01/21735
PRIORITY FILING DATE: 2001-07-09
PRIORITY APPLICATION NUMBER: US 60/219,556
PRIORITY FILING DATE: 2000-07-20
PRIORITY APPLICATION NUMBER: US 60/220,624
PRIORITY FILING DATE: 2000-07-25
PRIORITY APPLICATION NUMBER: US 60/220,664
PRIORITY FILING DATE: 2000-07-25
PRIORITY APPLICATION NUMBER: PCT/US00/20710
PRIORITY FILING DATE: 2000-07-28
PRIORITY APPLICATION NUMBER: US 60/222,695
PRIORITY FILING DATE: 2000-08-02
PRIORITY APPLICATION NUMBER: US 09/643,657
PRIORITY FILING DATE: 2000-08-17
PRIORITY APPLICATION NUMBER: PCT/US00/23522
PRIORITY FILING DATE: 2000-08-23
PRIORITY APPLICATION NUMBER: PCT/US00/23328
PRIORITY FILING DATE: 2000-08-24
PRIORITY APPLICATION NUMBER: US 60/230,978
PRIORITY FILING DATE: 2000-09-07
PRIORITY APPLICATION NUMBER: US 60/000,000
PRIORITY FILING DATE: 2000-09-15
PRIORITY APPLICATION NUMBER: US 09/664,610
PRIORITY FILING DATE: 2000-09-18
PRIORITY APPLICATION NUMBER: US 09/665,350
PRIORITY FILING DATE: 2000-09-18
PRIORITY APPLICATION NUMBER: US 60/242,922
PRIORITY FILING DATE: 2000-10-24
PRIORITY APPLICATION NUMBER: US 09/709,238
PRIORITY FILING DATE: 2000-11-08
PRIORITY APPLICATION NUMBER: PCT/US00/30952
PRIORITY FILING DATE: 2000-11-08
PRIORITY APPLICATION NUMBER: PCT/US00/30873
PRIORITY FILING DATE: 2000-11-10
PRIORITY APPLICATION NUMBER: PCT/US00/32678
PRIORITY FILING DATE: 2000-12-01
PRIORITY APPLICATION NUMBER: US 09/747,259
PRIORITY FILING DATE: 2000-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/34956
PRIORITY FILING DATE: 2000-12-20
PRIORITY APPLICATION NUMBER: US 09/767,609
PRIORITY FILING DATE: 2001-01-22
PRIORITY APPLICATION NUMBER: US 09/796,498
PRIORITY FILING DATE: 2001-02-28
PRIORITY APPLICATION NUMBER: PCT/US01/06520
PRIORITY FILING DATE: 2001-02-28
PRIORITY APPLICATION NUMBER: PCT/US01/06565
PRIORITY FILING DATE: 2001-03-01
PRIORITY APPLICATION NUMBER: US 09/802,736
PRIORITY FILING DATE: 2001-03-09
PRIORITY APPLICATION NUMBER: US 09/808,689
PRIORITY FILING DATE: 2001-03-14
PRIORITY APPLICATION NUMBER: US 09/816,744
PRIORITY FILING DATE: 2001-03-22
PRIORITY APPLICATION NUMBER: US 09/828,366
PRIORITY FILING DATE: 2001-04-05
PRIORITY APPLICATION NUMBER: US 09/854,208
PRIORITY FILING DATE: 2001-05-10
PRIORITY APPLICATION NUMBER: US 09/854,280
PRIORITY FILING DATE: 2001-05-10
PRIORITY APPLICATION NUMBER: US 09/866,028
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: US 09/866,034
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: PCT/US01/17092

PRIOR FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: US 09/870,574
PRIORITY FILING DATE: 2001-05-30
PRIORITY APPLICATION NUMBER: PCT/US01/17443
PRIORITY FILING DATE: 2001-05-30
PRIORITY APPLICATION NUMBER: PCT/US01/17800
PRIORITY FILING DATE: 2001-06-01
PRIORITY APPLICATION NUMBER: PCT/US01/19692
PRIORITY FILING DATE: 2001-06-20
PRIORITY APPLICATION NUMBER: PCT/US01/00000
PRIORITY FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 354
LENGTH: 179
TYPE: PRT
ORGANISM: Homosapiens
US-10-081-056-354

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAALQKSVSFLMCTLATSCLLILALLVQGGAAPISSHCHLDKSNFQPYITRTFMIA 60
Db 1 MAALQKSVSFLMCTLATSCLLILALLVQGGAAPISSHCHLDKSNFQPYITRTFMIA 60
Qy 61 KEASLADNNTDVRILIGELKFLHGVSMRRCYLMKQVLAFTLEVLFPQSDRFQPMQEVVP 120
Db 61 KEASLADNNTDVRILIGELKFLHGVSMRRCYLMKQVLAFTLEVLFPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDLIHQRNVQKLDIQRNVQKLDIQRNVQKLDIQRNVQKLDI 179
Db 121 FLARLSNRLSTCHIEGDDLIHQRNVQKLDIQRNVQKLDIQRNVQKLDIQRNVQKLDI 179

RESULT 9

US-10-219-535-244
Sequence 244, Application US/10219535
Publication No. US20040044179A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C60
CURRENT APPLICATION NUMBER: US/10/219,535
PRIORITY FILING DATE: 2002-08-14
PRIORITY APPLICATION NUMBER: 10/119,480
PRIORITY FILING DATE: 2002-04-09
PRIORITY APPLICATION NUMBER: 60/059113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/062287
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/063549
PRIORITY FILING DATE: 1997-10-28
PRIORITY APPLICATION NUMBER: 60/064103
PRIORITY FILING DATE: 1997-10-31
PRIORITY APPLICATION NUMBER: 60/069873
PRIORITY FILING DATE: 1997-12-17
PRIORITY APPLICATION NUMBER: 60/078910
PRIORITY FILING DATE: 1998-03-20
PRIORITY APPLICATION NUMBER: 60/079294
PRIORITY FILING DATE: 1998-03-25
PRIORITY APPLICATION NUMBER: 60/079656

```
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 244
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-535-244

Query Match      99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQOPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQOPYITNRTFMLA 60
Qy 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDLLHIQNVOKLDTVKKIGESGEIKAI GELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLLHIQNVOKLDTVKKIGESGEIKAI GELDLFMSLRNACI 179

RESULT 10
US-10-232-230-244
; Sequence 244, Application US/10232230
; Publication No. US20040044180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: 23530PIC103
; CURRENT APPLICATION NUMBER: US/10/232,230
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 244
; LENGTH: 179
```

```
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-230-244

Query Match      99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQOPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQOPYITNRTFMLA 60
Qy 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDLLHIQNVOKLDTVKKIGESGEIKAI GELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLLHIQNVOKLDTVKKIGESGEIKAI GELDLFMSLRNACI 179

RESULT 11
US-09-969-984-18
; Sequence 18, Application US/09969984
; Publication No. US20040048244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PP-0701-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,984
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/134,949; 60/144,270; 60/146,700; 60/157,508
; PRIOR FILING DATE: 1999-05-19; 1999-07-15; 1999-07-30; 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040048244A1 5571181CD1
US-09-969-984-18
```

```
Query Match      99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQOPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQOPYITNRTFMLA 60
Qy 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDLLHIQNVOKLDTVKKIGESGEIKAI GELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLLHIQNVOKLDTVKKIGESGEIKAI GELDLFMSLRNACI 179

RESULT 12
US-10-063-745-154
; Sequence 154, Application US/10063745
```

```
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-745-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
DB 1 MAALQKSVSFLMGTLATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGKLFHGVSMSECYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
DB 61 KEASLADNNTDVRLLIGKLFHGVSMSECYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGSGEIKALGELDLFMSLRNACI 179
DB 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGSGEIKALGELDLFMSLRNACI 179

RESULT 13
US-10-063-512-154
; Sequence 154, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-512-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
DB 1 MAALQKSVSFLMGTLATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGKLFHGVSMSECYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
DB 61 KEASLADNNTDVRLLIGKLFHGVSMSECYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGSGEIKALGELDLFMSLRNACI 179
DB 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGSGEIKALGELDLFMSLRNACI 179

RESULT 14
US-10-063-513-154
; Sequence 154, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-513-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
DB 1 MAALQKSVSFLMGTLATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGKLFHGVSMSECYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
DB 61 KEASLADNNTDVRLLIGKLFHGVSMSECYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGSGEIKALGELDLFMSLRNACI 179
DB 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGSGEIKALGELDLFMSLRNACI 179

RESULT 15
US-10-063-515-154
; Sequence 154, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-515-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
DB 1 MAALQKSVSFLMGTLATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGKLFHGVSMSECYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
DB 61 KEASLADNNTDVRLLIGKLFHGVSMSECYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGSGEIKALGELDLFMSLRNACI 179
DB 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGSGEIKALGELDLFMSLRNACI 179
```

```

; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-154

```

```

Query Match      99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQOPYITNRTFMLA 60
Db      1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQOPYITNRTFMLA 60

Qy      61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVINFTEEVLPFQSDRFQPMQEVVP 120
Db      61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVINFTEEVLPFQSDRFQPMQEVVP 120

Qy      121 FIARISNRLSTCHIEGDDLHIQRNVQKLDITVKKIGESGEIKAIIGELDLLFMSLENACI 179
Db      121 FLARISNRLSTCHIEGDDLHIQRNVQKLDITVKKIGESGEIKAIIGELDLLFMSLENACI 179

```

Search completed: June 30, 2004, 19:29:39
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:14:58 ; Search time 59 Seconds
(without alignments)
857.220 Million cell updates/sec

Title: US-10-050-552A-2
Perfect score: 903
Sequence: 1 MAALQKSVSSFLMTGLTSC.....EIKAIQELDLFWSLRNACI 179

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897	99.3	179	3	AAY92879 Human T C
2	897	99.3	179	3	AAB36292 Human GIL
3	897	99.3	179	4	AAB31210 Amino aci
4	897	99.3	179	4	AAB04538 Human cyt
5	897	99.3	179	4	AAB87602 Human PRO
6	897	99.3	179	4	AAB62664 Human IL-
7	897	99.3	179	4	AAB48074 Human ext
8	897	99.3	179	5	AAB37113 Human PRO
9	897	99.3	179	5	AAB19237 Human TIF
10	897	99.3	179	5	ABG95927 Human sec
11	897	99.3	179	5	ABB84993 Human PRO
12	897	99.3	179	5	AAB78081 Human int
13	897	99.3	179	5	AAB28608 Human IL-
14	897	99.3	179	5	AAB76909 Human int
15	897	99.3	179	5	ABB95599 Human arg
16	897	99.3	179	5	ABB79910 Human int
17	897	99.3	179	6	ABU80860 Human PRO
18	897	99.3	179	6	ABO25181 Novel hum
19	897	99.3	179	6	ABO33826 Novel hum
20	897	99.3	179	6	ABU90952 Novel hum
21	897	99.3	179	6	ABO34011 Human sec
22	897	99.3	179	6	ABU72028 Novel hum
23	897	99.3	179	6	ABU67299 Novel hum
24	897	99.3	179	6	ABU71582 Human sec
25	897	99.3	179	6	ABU72363 Human PRO

ALIGNMENTS

RESULT 1
AAY92879 AAY92879 standard; protein; 179 AA.
XX AC AAY92879;

XX AC AAY92879;
XX AC AAY92879;
XX 04-SEP-2000 (first entry)
XX DE Human T cell inducible factor.

XX TIF; T cell derived inducible factor; interleukin 9; STAT; IL-9;
XX Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;
XX chromosome 12q15.

XX Homo sapiens.

XX WO2000024758-A1.

XX 04-MAY-2000.

XX 18-OCT-1999; 99WO-US024424.

XX 26-OCT-1998; 98US-00178973.

XX 16-JUL-1999; 99US-00354243.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Dumoutier L, Loubhed J, Renauld J;

XX WPI; 2000-422495/36.

XX N-PSDB; AAB28839, AAB28840.

XX New nucleic acid molecule encoding a T cell derived inducible factor for treating asthma, an allergy or lymphoma.
XX Example 26; Fig 1; 46pp; English.

XX This is the human T cell derived inducible factor (TIF). The gene was mapped to chromosome 12q15. The human TIF was identified based on homology to a murine TIF, which was identified by subtraction cloning from a murine lymphoma cell line BW5147 in the presence or absence of interleukin 9 (IL-9). BW5147, can be grown in vitro, without the need to add any cytokines to its culture medium. Many IL-9 activities are mediated by activation of STAT transcription factors. The novel TIFs were expressed in the presence of IL-9, but not in its absence. TIFs induce STAT activation in cells. They can be used, e.g. in the stimulation of regeneration of targeted tissues. Their inhibitors or antagonists can be used to retard, prevent or inhibit differentiation of other tissues. The

ABU91036 Human PRO
ABO27357 Human sec
ABU72067 Novel hum
ABU67168 Novel hum
ABU92552 Human sec
ABU81222 Human sec
ABU82169 Novel hum
ABO53336 Novel hum
AAB30833 Human int
ABU98339 Novel hum
ABU89344 Novel hum
ABU82551 Novel hum
ABU96515 Human PRO
ABU72185 Human PRO
ABU79810 Human sec
ABJ72349 Human PRO
ABJ17211 Human tra
ABO44315 Human sec
ADA20016 Novel hum
ABU17399 Human tra

CC TIPS and their coding sequences are useful in the treatment of asthma,
 CC allergies and lymphoma (claimed). They are also useful for identifying
 CC compounds that inhibit or activate T cell induced factor activity in a
 CC cell (claimed)
 XX
 SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 3; Length 179;
 Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALOKSVSSFLMGTLATSCILLALLVOGGAAAPISSHCRDLKSNFQPPYITNRTFMLA 60
 DB 1 MAALOKSVSSFLMGTLATSCILLALLVOGGAAAPISSHCRDLKSNFQPPYITNRTFMLA 60
 QY 61 KEASLADNNTDRLIGEKLFHGVMSERCYLMKQVNFLEVLFPQSDRFPQYMQEVPV 120
 DB 61 KEASLADNNTDRLIGEKLFHGVMSERCYLMKQVNFLEVLFPQSDRFPQYMQEVPV 120
 QY 121 FIARISNRLSTCHIEGDDIHIQRNVQKLDVTVKKLGESGEIKAIKGLDILLFMSLRNACI 179
 DB 121 FIARISNRLSTCHIEGDDIHIQRNVQKLDVTVKKLGESGEIKAIKGLDILLFMSLRNACI 179

RESULT 2
 AAB36292
 ID AAB36292 standard; protein; 179 AA.
 AC AAB36292;
 DT 23-FEB-2001 (first entry)
 DE Human GIL-19/AE289 protein sequence.

Human; GIL-19/AE289; IL-10; Interleukin-10; nutrition;
 cell proliferation; immune stimulation; immune suppression;
 haematopoiesis regulation; tissue growth; inflammation; cancer.
 Homo sapiens.
 WC200065027-A2.
 02-NOV-2000.
 28-APR-2000; 2000WO-US011479.
 28-APR-1999; 99US-0131473P.
 (GEMY) GENETICS INST INC.
 Jacobs K, Fouser L, Spaulding V, Xuan D;
 WPI; 2000-687325/67.
 N-PSDB; AAC81773.

Human GIL-19 protein that shows a high degree of homology to IL
 (interleukin)-10, useful in upregulation of humoral immune responses, as
 an anti-inflammatory agent and as a modulator of immune responses
 associated with injury.
 Claim 9; Page 59-60; 60pp; English.
 The present invention provides the protein and coding sequences for the
 novel human GIL-19/AE289 protein. The protein shows homology to
 interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used in
 the regulation of cell proliferation and differentiation, haematopoiesis,
 immune stimulation or suppression, tissue growth and tumour inhibition.
 In addition, it also has uses in the treatment of inflammation and in
 nutrition
 Sequence 179 AA;
 Query Match 99.3%; Score 897; DB 3; Length 179;

Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAALOKSVSSFLMGTLATSCILLALLVOGGAAAPISSHCRDLKSNFQPPYITNRTFMLA 60
 DB 1 MAALOKSVSSFLMGTLATSCILLALLVOGGAAAPISSHCRDLKSNFQPPYITNRTFMLA 60
 QY 61 KEASLADNNTDRLIGEKLFHGVMSERCYLMKQVNFLEVLFPQSDRFPQYMQEVPV 120
 DB 61 KEASLADNNTDRLIGEKLFHGVMSERCYLMKQVNFLEVLFPQSDRFPQYMQEVPV 120
 QY 121 FIARISNRLSTCHIEGDDIHIQRNVQKLDVTVKKLGESGEIKAIKGLDILLFMSLRNACI 179
 DB 121 FIARISNRLSTCHIEGDDIHIQRNVQKLDVTVKKLGESGEIKAIKGLDILLFMSLRNACI 179

RESULT 3
 AAB31210
 ID AAB31210 standard; protein; 179 AA.
 AC AAB31210;
 DT 20-APR-2001 (first entry)

Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
 PRO185; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
 PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
 PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
 PRO246; PRO285; PRO941; PRO10996; PRO6003; PRO6004; PRO350; PRO2630;
 PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
 Homo sapiens.
 Key Location/Qualifiers
 Peptide 1..33 /note= "signal peptide"
 Modified-site 14..20 /note= "N-myristoylation site"
 Modified-site 54..58 /note= "N-glycosylation site"
 Modified-site 68..72 /note= "N-glycosylation site"
 Modified-site 82..88 /note= "N-glycosylation site"
 Modified-site 97..10 /note= "N-myristoylation site"
 Modified-site /note= "N-glycosylation site"

WO200077037-A2.
 21-DEC-2000.
 22-MAY-2000; 2000WO-US014042.
 15-JUN-1999; 99US-0139695P.
 20-JUL-1999; 99US-0145070P.
 26-JUL-1999; 99US-0145698P.
 17-AUG-1999; 99US-0149396P.
 01-SEP-1999; 99WO-US020111.
 08-SEP-1999; 99WO-US020594.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028565.
 07-DEC-1999; 99US-0169495P.
 05-JAN-2000; 2000WO-US000219.
 18-FEB-2000; 2000WO-US004341.
 22-FEB-2000; 2000WO-US004342.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.

PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 98US-016949P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 21-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2001-183260/18.
DR N-PSDB; AAF92134.
XX
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 12; Fig 154; 278pp; English.
XX
CC The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX
SQ Sequence 179 AA;
Query Match 99.3%; Score 897; DB 4; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAALQKSVSFLMGTATSCILLALLVQGGAAAPISCHCLDKSNFQOPIYTRTFMLA 60
Db 1 MAALQKSVSFLMGTATSCILLALLVQGGAAAPISCHCLDKSNFQOPIYTRTFMLA 60
Qy 61 KEASLADNDTVRLIGEKLFHGVSMSECYLMKQVNFLEVLFPQSDRFQPMQEVVP 120
Db 61 KEASLADNDTVRLIGEKLFHGVSMSECYLMKQVNFLEVLFPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDHIIQNVQKIKDTVKKIGSGEIKATGELDLFMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDHIIQNVQKIKDTVKKIGSGEIKATGELDLFMSLRNACI 179
RESULT 6
AAB62664
ID AAB62664 standard; protein; 179 AA.
XX
AC AAB62664;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human IL-TIF polypeptide.
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;

KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW immunosuppressive; chromosome 6q24.1-25.2; human.
XX
OS Homo sapiens.
XX
PN WO200104067-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032703.
XX
PR 03-DEC-1999; 99US-0169049P.
PR 13-SEP-2000; 2000US-0232219P.
PR 31-OCT-2000; 2000US-0244610P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2001-356158/37.
DR N-PSDB; AAF83741.
XX
XX New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions.
PT
XX
PS Example 17; Page 195-196; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing IL-
CC TIF induced or IL-9 induced inflammation; and suppressing an inflammatory
CC response in a mammal with inflammation. Heteromeric/ multimeric receptor
CC polypeptides such as soluble zcytor 16/CRF2-4 can be used to reduce
CC progression and symptoms of cancer. Zcytor16 polypeptides can also be
CC used to detect IL-TIF levels which is indicative of pathological
CC conditions including inflammatory states (e.g. rheumatoid arthritis) and
CC cancer. Antibodies that bind zcytor16 polypeptides and the polypeptides
CC themselves are useful for the treatment of inflammation, inflammatory
CC diseases (e.g. infection, asthma, inflammatory bowel disease, rheumatoid
CC arthritis and atherosclerosis) and autoimmune diseases. The antibodies
CC and zcytor16 polynucleotides are also useful for detecting cancer. The
CC present sequence represents the human IL-TIF protein
XX
SQ Sequence 179 AA;
Query Match 99.3%; Score 897; DB 4; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAALQKSVSFLMGTATSCILLALLVQGGAAAPISCHCLDKSNFQOPIYTRTFMLA 60
Db 1 MAALQKSVSFLMGTATSCILLALLVQGGAAAPISCHCLDKSNFQOPIYTRTFMLA 60
Qy 61 KEASLADNDTVRLIGEKLFHGVSMSECYLMKQVNFLEVLFPQSDRFQPMQEVVP 120
Db 61 KEASLADNDTVRLIGEKLFHGVSMSECYLMKQVNFLEVLFPQSDRFQPMQEVVP 120
Qy 121 FIARISNRLSTCHIEGDDHIIQNVQKIKDTVKKIGSGEIKATGELDLFMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDHIIQNVQKIKDTVKKIGSGEIKATGELDLFMSLRNACI 179
RESULT 7
AAB48074
ID AAB48074 standard; protein; 179 AA.
XX
AC AAB48074;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human extracellular signaling molecule (EXCS) (ID 5571181CDI).

XX Extracellular signaling molecule; EXCS; anti-inflammatory; human;
 KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
 KW viricide; antibacterial; anti-HIV; human immunodeficiency virus;
 KW antinfertility; cerebroprotective; nootropic; antitumor; antifungal;
 KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
 KW keratolytic; protozoacide; gene therapy.
 XX Homo sapiens.
 OS
 XX
 XX WO200070049-A2.
 XX
 XX 23-NOV-2000.
 XX
 XX 19-MAY-2000; 2000WO-US013975.
 XX
 XX 19-MAY-1999; 99US-0134949P.
 XX 15-JUL-1999; 99US-0144270P.
 XX 30-JUL-1999; 99US-0146700P.
 XX 04-OCT-1999; 99US-0157508P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
 PI Azimzai Y, Lu DAM, Patterson C;
 XX
 XX WPI: 2001-025021/03.
 XX N-PSDB; AAC84310.
 XX
 XX New human extracellular signaling nucleic acids and polypeptides useful
 PT for diagnosing, treating and preventing infections and gastrointestinal,
 PT neurological, reproductive, and autoimmune/inflammatory disorders.
 XX
 XX Claim 1; Page 94; 114pp; English.
 XX
 XX The invention provides human extracellular signaling molecules (EXCS) and
 CC polynucleotides which identify and encode EXCS. EXCS can be expressed by
 CC standard recombinant methodology. The amino acid and nucleic acid
 CC sequences of EXCS are useful for diagnosing, treating and preventing
 CC infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis),
 CC neurological (e.g. epilepsy, ischemic cerebrovascular disease, stroke),
 CC reproductive (infertility, ovulatory defects, endometriosis), autoimmune
 CC /inflammatory (actinic keratosis, acquired immunodeficiency syndrome
 CC (AIDS), Addison's disease), and cell proliferative disorders including
 CC cancers (of the breast, adrenal gland, bone). They may also be used to
 CC treat fatal familial insomnia, nutritional and metabolic diseases of the
 CC nervous system, myopathies, mental disorders (anxiety, schizophrenia,
 CC mood), as well as infections caused by parasites (malaria, leishmania,
 CC trypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial
 CC (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus,
 CC blastomycosis, dermatophytes) agents. The nucleic acids, polypeptides,
 CC antagonists, agonists, pharmaceutical compositions, and antibodies may
 CC also be used for treating or preventing disorders associated with
 CC increased or decreased expression or activity of EXCS. EXCS
 CC polynucleotides may also be used to detect and quantify gene expression
 CC in biopsied tissues in which expression of EXCS may be correlated with
 CC the disease, to determine presence or excess expression of EXCS, to
 CC monitor regulation of EXCS levels during therapeutic intervention, to
 CC detect the presence of associated disorders, as targets in microarray, to
 CC generate hybridization probes, and to detect differences in gene
 CC sequences among normal, carrier or affected individuals. Antibodies may
 CC also be used in diagnosing disorders, in monitoring patients being
 CC treated with EXCS agonists, antagonists or inhibitors. Sequences AAB48057
 CC -B48082 represent the EXCS of the invention
 XX
 XX Sequence 179 AA;
 XX
 XX Query Match 99.3%; Score 897; DB 4; Length 179;
 XX Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 XX Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 MAALQKSVSFLMGTATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
 |||

Db 1 MAALQKSVSFLMGTATSCILLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFMLA 60
 Qy 61 KEASLADNNTDVRLLIGEKLFHGVSMSECYLMKQVNFLLSEVLPQSDRFPQYMOEYVVP 120
 |||
 Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSECYLMKQVNFLLSEVLPQSDRFPQYMOEYVVP 120
 |||
 Qy 121 FIARISNRLSTCHTEGDDLHQRNVQKLTQVKKIGESGEIKAGELDLFMSLRNACI 179
 |||
 Db 121 FLARLSNRLSTCHTEGDDLHQRNVQKLTQVKKIGESGEIKAGELDLFMSLRNACI 179
 |||
 RESULT 8
 AAU83713
 ID AAU83713 standard; protein; 179 AA.
 XX
 AC AAU83713;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 244.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 XX WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US021066.
 XX
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220585P.
 PR 25-JUL-2000; 2000US-0220605P.
 PR 25-JUL-2000; 2000US-0220607P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220638P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 25-JUL-2000; 2000US-0220666P.
 PR 26-JUL-2000; 2000US-0220893P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-AUG-2000; 2000US-022425P.
 PR 22-AUG-2000; 2000US-0227133P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 XX WPI: 2002-172001/22.
 XX N-PSDB; AEX33657.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX

PS Claim 11; Fig 244; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX
SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALQKSVSSFLMGTLATSCILLALLVGGGAAAPISSHCRDLKSNFQOPIYTNRTFMLA 60
DB 1 MAALQKSVSSFLMGTLATSCILLALLVGGGAAAPISSHCRDLKSNFQOPIYTNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSECYLMKQVNLFTLEVLFPQSDRFPQYMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSECYLMKQVNLFTLEVLFPQSDRFPQYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHQVOKLQDTVKKIGESGEIKAI GELDLFMSLRNACI 179
DB 121 FIARISNRLSTCHIEGDDHLHQVOKLQDTVKKIGESGEIKAI GELDLFMSLRNACI 179

RESULT 9
AAE19237
ID AAE19237 standard; protein; 179 AA.
XX
AC AAE19237;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human TIF protein.
XX
KW T cell derived inducible factor; TIF; interleukin-21; IL-21; human;
KW STAT transcription factor; acute phase protein; inflammation;
KW Chromosome 12.
XX
OS Homo sapiens.
XX
FN WO200210393-A2.
XX
PD 07-FEB-2002.
XX
PF 27-JUN-2001; 2001WO-US020485.
XX
PR 27-JUL-2000; 2000US-00626617.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Dumoutier L, Renaud J;
XX
DR W2; 2002-195964/25.
DR N-PSDB; AAD30645.
XX
PT Stimulating expression of STAT transcription factor and inducing
PT production of acute phase protein in a cell, involves contacting a cell
PT capable of expressing STAT with T cell derived inducible factors.
XX

PS Disclosure; Page 64; 64pp; English.
XX
CC The invention relates to nucleic acid molecules encoding T cell derived
CC inducible factors (TIFs) also known as interleukin-21 (IL-21). TIF
CC polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or IL-21
CC molecules are implicated in activation of STAT transcription factors,
CC acute phase proteins and inflammation. The present sequence is human TIF
CC protein. The TIF gene is located on chromosome 12
XX
SQ Sequence 179 AA;
Query Match 99.3%; Score 897; DB 5; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALQKSVSSFLMGTLATSCILLALLVGGGAAAPISSHCRDLKSNFQOPIYTNRTFMLA 60
DB 1 MAALQKSVSSFLMGTLATSCILLALLVGGGAAAPISSHCRDLKSNFQOPIYTNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSECYLMKQVNLFTLEVLFPQSDRFPQYMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSECYLMKQVNLFTLEVLFPQSDRFPQYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHQVOKLQDTVKKIGESGEIKAI GELDLFMSLRNACI 179
DB 121 FIARISNRLSTCHIEGDDHLHQVOKLQDTVKKIGESGEIKAI GELDLFMSLRNACI 179
RESULT 10
ABG95927
ID ABG95927 standard; protein; 179 AA.
XX
AC ABG95927;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human secreted/transmembrane protein PRO10096.
XX
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
FN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 10-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 11-JUN-1998; 98US-0088825P.
PR 12-JUN-1998; 98US-0088863P.
PR 16-JUN-1998; 98US-0089105P.
PR 17-JUN-1998; 98US-0089514P.
PR 19-JUN-1998; 98US-0089653P.
PR 22-JUN-1998; 98US-0089952P.
PR 24-JUN-1998; 98US-0090446P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.

KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.

XX WO2000200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0223695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 03-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00767608.

XX 28-FEB-2001; 2001US-00796498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 30-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017443.

XX 01-JUN-2001; 2001WO-US017830.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;
 XX Godowski EJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.
 XX N-PSDB; ABL88248.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 354; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABL8817 to
 XX ABL88503. The PRO proteins and polynucleotides have cardiant, cytostatic,
 XX antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 XX activities, and can be used in gene therapy. The PRO polynucleotides,
 XX proteins, agonists and antagonists are useful for treating or diagnosing
 XX a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 XX atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 XX angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
 XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 XX healing. The PRO polynucleotides have applications in molecular biology,

CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention

XX Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;
 Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAAALOKSVSSFLMGLTATSCLLLLALLVOGAAAPISSHCRDLKSNFQDPYITNRTFMLA 60
 DB 1 YAAALOKSVSSFLMGLTATSCLLLLALLVOGAAAPISSHCRDLKSNFQDPYITNRTFMLA 60

QY 61 KEASLADNNTDVLRLGKLFHGVSMSERCYLMKQVLFNFTLEVLFPQSDRFPQYMEVVP 120
 DB 61 KEASLADNNTDVLRLGKLFHGVSMSERCYLMKQVLFNFTLEVLFPQSDRFPQYMEVVP 120

QY 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKLGESGEIKAIKIGELDLFWSLRNACI 179
 DB 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKLGESGEIKAIKIGELDLFWSLRNACI 179

RESULT 12
 AAU78081
 ID AAU78081 standard; protein; 179 AA.

XX AAU78081;
 XX 05-JUN-2002 (first entry)

XX Human interleukin 22 (IL-22) protein sequence.

XX Interleukin 22; IL-22; cytostatic; antiinflammatory; IL-22 antagonist;
 XX immunotherapy; PAPI; pancreatitis associated protein; receptor; IL-22R;
 XX IL-10Rbeta; bioactive molecule linkage; cell death; pancreatitis;
 XX pancreatic disorder; pancreatic carcinoma; acinar cell carcinoma; human;
 XX mixed cell population pancreatic carcinoma.

XX Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..33
 FT Modified-site /label= Signal_peptide
 FT Modified-site /note= "Asn is N-myristolated"

FT Protein 34..179
 FT Modified-site /label= Mature_human_interleukin_22_(IL_22)

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

PT Novel isolated interleukin 22 polypeptide useful for identifying IL-22
PT agonists and antagonists that are used for treating acute pancreatitis,
PT chronic pancreatitis, pancreatic carcinoma.

XX Claim 11; Fig 2; 94pp; English.

PS The present invention relates to a new polypeptide having at least 80%
CC identity to a 101 amino acid interleukin (IL)-22 sequence. The invention
CC is useful for detecting IL-22R (IL-22 receptor) or IL-10Rbeta polypeptide
CC in a sample which involves contacting sample with an IL-22 polypeptide
CC and determining the formation of an IL-22R/IL-22 polypeptide conjugate or
CC an IL-10Rbeta/IL-22 polypeptide conjugate. Preferably, the IL-22
CC polypeptide is labelled with a detectable label or is attached to a solid
CC support. The polypeptide is also useful for linking a bioactive molecule,
CC e.g. toxin, radiolabel or antibody that causes the death of the cell, to
CC a cell expressing IL-22R polypeptide or IL-10Rbeta polypeptide which
CC involves contacting the cell with IL-22 polypeptide that is bound to the
CC bioactive molecule and allowing binding of the IL-22 polypeptide with IL-
CC 22R or IL-10Rbeta polypeptide thus linking the bioactive molecules to the
CC cell. The molecules of the invention can also be used for modulating
CC biological activity of cell expressing IL-22R or IL-10Rbeta polypeptide,
CC whereby the cell is killed and the antibody of the invention is useful
CC for inhibiting IL-22 induced expression of PAP1 (pancreatitis associated
CC protein) by pancreatic cells. The antibody is also useful for treating a
CC pancreatic disorder such as acute or chronic pancreatitis, pancreatic
CC carcinoma including acinar cell carcinoma or mixed cell population
CC of pancreatic carcinoma and for reducing the activated or inflamed condition
CC of the pancreas in a mammal. The present amino acid sequence represents
CC the human interleukin 22 (IL-22) protein of the invention

XX Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRDKSNFQOPIYINRTFMLA 60
DB 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRDKSNFQOPIYINRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPMQVWP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPMQVWP 120
QY 121 FIARISNRLSTCHIEGDDLIHQNVQKLDKTVKKGESGIIKAIIGELDLFLFMSLRNACI 179
DB 121 FLARLSNRLSTCHIEGDDLIHQNVQKLDKTVKKGESGIIKAIIGELDLFLFMSLRNACI 179

RESULT 13

AAE28608
ID AAE28608 standard; protein; 179 AA.

XX AAE28608;

DT 27-DEC-2002 (first entry)

DE Human IL-TIF protein #1.

XX Cytokine receptor; Zcytor16; IL-TIF; autoimmune disease; dermatological;
XX inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;
XX asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;
XX diabetes; atherosclerosis; glomerulonephritis; gene therapy; cytostatic;
XX immunosuppressive; nephrotropic; allergy; placental health; abortion;
XX cancer; human.

OS Homo sapiens.

XX W0200270655-A2.

PD 12-SEP-2002.

XX 04-MAR-2002; 2002WO-US006267.

XX 02-MAR-2001; 2001US-0273035P.
PR 27-MAR-2001; 2001US-0279232P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Xu W, Kindsvoegel W, Chen Z;

XX WPI; 2002-698750/75.

XX N-PSDS; AAD45964.

PT New Zcytor16 polypeptide useful for treating autoimmune or inflammatory
PT diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma,
PT atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects
PT of IL-TIF.

PS Disclosure; Page 197-198; 221pp; English.

XX The invention relates to cytokine receptor designated as mouse Zcytor16
CC which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is
CC useful in modulating the immune system by binding Zcytor16 ligand, and
CC thus, preventing the binding of the ligand with endogenous Zcytor16
CC receptor. It is useful for studying human inflammation or immune
CC function, or for treating autoimmune or inflammatory diseases such as
CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus
CC erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer,
CC diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic
CC aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-
CC Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the
CC anti-mouse Zcytor16 antibody are useful as probes in detecting gene
CC expression and gene structure, such as in the diagnosis and/or prevention
CC of spontaneous abortions or in monitoring placental health and function.
CC It is also used in gene therapy. The present sequence is human IL-TIF
CC protein

XX Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRDKSNFQOPIYINRTFMLA 60
DB 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRDKSNFQOPIYINRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPMQVWP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPMQVWP 120
QY 121 FIARISNRLSTCHIEGDDLIHQNVQKLDKTVKKGESGIIKAIIGELDLFLFMSLRNACI 179
DB 121 FLARLSNRLSTCHIEGDDLIHQNVQKLDKTVKKGESGIIKAIIGELDLFLFMSLRNACI 179

RESULT 14

AAU76909

ID AAU76909 standard; protein; 179 AA.

XX AAU76909;

XX 05-JUN-2002 (first entry)

XX Human interleukin-T-cell inducible factor (IL-TIF).

XX Z-Cytor II; human; cytokine receptor; atopy; psoriasis;
XX interleukin-T-cell inducible factor; IL-TIF; allergy; asthma;
XX receptor-modulated apoptosis; Th1; immune response; pancreatitis;
XX type I diabetes; IDDM; pancreatic cancer; Graves disease; SLE;
XX inflammatory bowel disease; IBD; Crohn's disease; colon cancer;
XX intestinal cancer; diverticulosis; autoimmune disease; sepsis;
XX multiple sclerosis; MS; systemic lupus erythematosus; myasthenia gravis;
XX rheumatoid arthritis; kidney dysfunction.

OS Homo sapiens.
 XX WO200212345-A2.
 XX 14-FEB-2002.
 XX 08-AUG-2001; 2001WO-US024838.
 XX 08-AUG-2000; 2000US-0223827P.
 PR 01-DEC-2000; 2000US-0250876P.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Kindsvogel WR, Topouzis S;
 PI WPI; 2002-217182/27.
 XX N-PSDB; ABK10503.
 XX New soluble cytokine receptor which binds interleukin-T-cell inducible
 PT factor and antagonizes its activity in inflammatory and immune diseases
 PT such as cancer, diabetes, asthma, sepsis, psoriasis and autoimmune
 PT diseases.
 XX
 XX Example 1; Page 98; 117pp; English.
 XX
 CC This invention relates to the protein and cDNA sequences of a novel
 CC soluble cytokine receptor polypeptide designated zcytorII, which binds
 CC interleukin-T-cell inducible factor (IL-TIF) or antagonizes IL-TIF
 CC activity. The protein of the invention is useful for reducing IL-TIF- or
 CC IL-9 induced inflammation, and inhibiting IL-TIF-induced proliferation.
 CC The protein is also useful for suppressing an immune response in a mammal
 CC exposed to an antigen or pathogen. Soluble zcytorII receptor or
 CC heterodimeric polypeptide is useful for enhancing the in vivo killing of
 CC target tissues by directly stimulating a zcytorII receptor-modulated
 CC apoptotic pathway. IL-TIF is involved in promoting Th1-type immune
 CC responses and antagonists of IL-TIF have beneficial use against diseases
 CC involving such immune responses. Soluble zcytorII heterodimers are useful
 CC as antagonists in inflammatory and immune diseases or conditions such as
 CC pancreatitis, type I diabetes (IDDM), pancreatic cancer, Graves disease,
 CC inflammatory bowel disease (IBD), Crohn's disease, colon and intestinal
 CC cancer, diverticulosis, autoimmune disease (e.g. IDDM, multiple sclerosis
 CC (MS), systemic lupus erythematosus (SLE), myasthenia gravis, rheumatoid
 CC arthritis and IBD), sepsis, asthma, allergy and other atopic diseases,
 CC psoriasis and kidney dysfunction. Soluble zcytorII receptor or
 CC heterodimeric receptor polypeptides are useful in vivo or in diagnostic
 CC applications to detect IL-TIF expressing cancers in vivo or in tissue
 CC samples and to prepare antibodies. ZcytorII serves as a target for Mab
 CC therapy of cancer where an antagonising Mab inhibits cancer growth and
 CC targets immune-mediated killing. The present sequence represents the
 CC interleukin-T-cell inducible factor (IL-TIF) protein, the activity of
 CC this protein is inhibited by the ZcytorII protein of the invention
 XX
 SQ Sequence 179 AA;
 Query Match 99.3%; Score 897; DB 5; Length 179;
 Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISSHCRIDKSNFQPPVITNRFTMLA 60
 Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAAPISSHCRIDKSNFQPPVITNRFTMLA 60
 Qy 61 KEASLADNNTVRLIGEKLFHGVSMSECYLMKQVNLFTLEVLFPQSDRFPQYMQEYVP 120
 Db 61 KEASLADNNTVRLIGEKLFHGVSMSECYLMKQVNLFTLEVLFPQSDRFPQYMQEYVP 120
 Qy 121 FIARISNRLSTCHIEGDDHLHQRNVQKLDVTVKKIGESGEIKAIQELDLFWSLRNACI 179
 Db 121 FLARLSNRLSTCHIEGDDHLHQRNVQKLDVTVKKIGESGEIKAIQELDLFWSLRNACI 179
 RESULT 15
 ABB95599

AB95599 standard; protein; 179 AA.
 ABB95599;
 19-JUL-2002 (first entry)
 Human angiogenesis related protein PRO10096 SEQ ID NO: 354.
 Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 cardiact; cytostatic; antiangiogenic; hypotensive; vulnerary;
 antiarteriosclerotic.
 Homo sapiens.
 WO200208284-A2.
 31-JAN-2002.
 09-JUL-2001; 2001WO-US021735.
 20-JUL-2000; 2000US-0219556P.
 25-JUL-2000; 2000US-0220624P.
 25-JUL-2000; 2000US-0220664P.
 28-JUL-2000; 2000WO-US020710.
 02-AUG-2000; 2000US-0222695P.
 17-AUG-2000; 2000US-00643657.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 07-SEP-2000; 2000US-0230978P.
 18-SEP-2000; 2000US-00664610.
 18-SEP-2000; 2000US-00665350.
 24-OCT-2000; 2000US-0242922P.
 08-NOV-2000; 2000US-00709238.
 08-NOV-2000; 2000WO-US030952.
 10-NOV-2000; 2000WO-US030873.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000US-00747259.
 20-DEC-2000; 2000WO-US034956.
 22-JAN-2001; 2001US-00767609.
 28-FEB-2001; 2001US-00796498.
 28-FEB-2001; 2001WO-US006520.
 01-MAR-2001; 2001WO-US006666.
 09-MAR-2001; 2001US-00802706.
 14-MAR-2001; 2001US-00808689.
 22-MAR-2001; 2001US-00816744.
 05-APR-2001; 2001US-00828366.
 10-MAY-2001; 2001US-00854208.
 10-MAY-2001; 2001US-00854280.
 25-MAY-2001; 2001US-00866028.
 25-MAY-2001; 2001WO-US017092.
 30-MAY-2001; 2001US-00870574.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PACINI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye M;
XX WPI; 2002-171999/22.
DR N-PSDB; ABL95737.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 354; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
XX Sequence 179 BA;
SQ
Query Match 99.3%; Score 897; DB 5; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALOKSVSEFLMGTLATSCLLLLALLVOGGAAPISSHCHLDKSNFQPYITNRTFMLA 60
Db 1 MAALOKSVSEFLMGTLATSCLLLLALLVOGGAAPISSHCHLDKSNFQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEWVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEWVP 120
QY 121 FIARISNRLSTCHIEGDDLIHQNVOKLQDTVKKIGESGEIKAIGBLDLLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLIHQNVOKLQDTVKKIGESGEIKAIGBLDLLFMSLRNACI 179

Search completed: June 30, 2004, 19:28:45
Job time : 62 secs